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## ALIGNMENTS

30L 373		AA DE Human colon cancer antigen protein SEQ ID NO:4718. vv	AA Kwman; colon cancer; colon cancer antigen; diagnosis; detection; KW colorectal carcinoma.	XX OS Homo sapiens.	XX PN WO200122920-A2.	XX PD 05-APR-2001.	XX PF 28-SEP-2000; 2000WO-US026524.	AX 29-SEP-1999; 99US-0157137P. PR 03-NOV-1999; 99US-0163280P.	XX PA (HUMA-) HUMAN GENOME SCI INC.	AX PI Ruben SM, Barash SC, Birse CE, Rosen CA;	XX DR WPI; 2001-235357/24. DR N-PSDB; AAH33385.	AX PT Pucleic acids encoding 4277 human colon cancer-associated polypeptides, PT useful for preventing, diagnosing and/or treating colorectal cancers.	XX PS Claim 11; Page 6520-6521; 9803pp; English.	AAH32943 to AAH37195 and AAG73514 to AAG77788 represent hu cancer-associated nucleic acid molecules (N) and proteins proteins are collectively known as colon cancer antigens. cancer antigens have cytostatic activity and can be used and vaccine production. N and P may be used in the prevent and treatment of diseases associated with inappropriate P axample. N and P may be used to treat disorders associated by and P may be used to treat disorders associated	1 m	n; 436 AA.  In protein SEQ ID NO:4718.  In cancer antigen; diagnosis; detection;  in cancer antigen; diagnosis; detection;  37P.  80P.  INC.  INC.  INC.  INC.  INC.  INC.  AAG73514 to AAG77788 represent human colon acid molecules (N) and proteins (P), where the known as colon cancer antigens. The colon acid molecules (N) and proteins (P), where the known as colon cancer antigens. The colon stataic activity and can be used in gene therapy istait activity and can be used in gene therapy associated with inappropriate P expression. For sea to treat disorders associated with decreased mutations or deletions in a patient's genome of P by expressing inactive proteins or to war production of P. Additionally, N may be used with inappropriate with any be used with season; and patient's genome of P by expressing inactive proteins or to mutations or deletions in a patient's genome of P by expressing inactive proteins or to man production of P. Additionally, N may be used war production of P. Additionally, N may be used
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Nucleic acids encoding 4277 human colon cancer-associated useful for preventing, diagnosing and/or treating colorect Claim 11; Page 6520-6521; 9803pp; English.  AAH22943 to AAH37195 and AAG73514 to AAG77788 represent hucancer-associated nucleic acid molecules (N) and proteins proceins are collectively known as colon cancer antigens. Cancer antigens have cytostatic activity and can be used in and vaccine production. N and P may be used in the prevent and treatment of diseases associated with inappropriate P example. N and P may be used to treat disorders associated that affect the activity of P by expressing inactive protes supplement the patients on production of P. Additionally, supplement	WPI; 2001-235357/24.  N-PSDB; AAH33385.  Nucleic acids encoding 4277 human colon cancer-associated useful for preventing, diagnosing and/or treating colorect Claim 11; Page 6520-6521; 9803pp; English.  AAH32943 to AAH37195 and AAG73514 to AAG77788 represent hucancer-associated nucleic acid molecules (N) and proteins proteins are collectively known as colon cancer antigens have cytostatic activity and can be used and vaccine production. N and P may be used in the prevent and treatment of diseases associated with inappropriate P example, N and P may be used to treat disorders associated expression by rectifying mutations or deletions in a patie that affect the activity of P by expressing inactive protest supplement the patients own production of P. Additionally, supplement the patients own production of P. Additionally,	Nucleic acids encoding 4277 human colon cancer-associated useful for preventing, diagnosing and/or treating colorect Claim 11; Page 6520-6521; 9803pp; English.  AAH32943 to AAH37195 and AAG73514 to AAG77788 represent hu cancer-associated nucleic acid molecules (N) and proteins proteins are collectively known as colon cancer antigens. cancer antigens have cytostatic activity and can be used and vaccine production. N and P may be used in the prevent and treatment of diseases associated with inappropriate P example. N and P may be used to treat disorders associated example, N and P may be used to treat disorders associated example. The activity of P by expressing inactive proteins upplement the patients own production of P. Additionally, supplement the patients own production of P. Additionally,	Claim 11; Page 6520-6521; 9803pp; English.  AAH32943 to AAH37195 and AAG73514 to AAG77788 represent hu cancer-associated nucleic acid molecules (N) and proteins proteins are collectively known as colon cancer antigens. Cancer antigens have cytostatic activity and can be used and vaccine production. N and P may be used in the prevent and treatment of diseases associated with inappropriate P example, N and P may be used to treat disorders associated example, N and P may be used to treat disorders associated that affect the activity of P by expressing inactive protesting applement the patients own production of P. Additionally, supplement the patients own production of P. Additionally,	AAH32943 to AAH37195 and AAG73514 to AAG77788 represent hu cancer-associated nucleic acid molecules (N) and proteins proteins are collectively known as colon cancer antigens. cancer antigens have cytostatic activity and can be used and vaccine production. N and P may be used in the prevent and treatment of diseases associated with inappropriate P example, N and P may be used to treat disorders associated expression by rectifying mutations or deletions in a patie that affect the activity of P by expressing inactive protestuplement the patients own production of P. Additionally,	expression by rectifying mutations or deletions that affect the activity of P by expressing inac supplement the patients own production of P. Add.	cell and	Fs, by inserting the nucleic to express the proteins. N $\delta$

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autolimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolyfic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 6q25.2-26,
                                                                                                                                                                                                                                           Gaps
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Weng G;
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Asundi V, Wang 2,
                                                                                                                                                                                                                                                                                                                          184 EREKEÇMMREKEELMLRLÓDYEEKTKKAERELSEGIGRALG 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel polypeptide sequence, SEQ ID NO:1712.
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Wang D, Ma Y, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2003 (first entry)
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Matches 40; Conservative
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                                                                                                                                                        Sequence 436 AA;
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candorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the carrying out the methods of the carrying out the methods for the interference of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC313661-ADC32627) and the polypeptides encoded by the contigs (ADC32628 - ADC33394). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the useful in diagnostics, and polypeptides of the invention are captured of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and anino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primares, and in the recombinant production of a proterion. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence of the invention note: The sequence of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 EREKEÇMMREKEELMLRLQDYEEKTKKAERELSEÇIQRALQ 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BREKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Protein P15311, SEQ ID NO 9933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE63987 standard; protein; 585 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 97.6 es 40; Conservative
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(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-268312/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 579 AA;
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The invention discloses a composition comprising two or more isolated rate or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the movel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a chart issue of a first animal control is differentially expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the cativity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating compound that a pain an approach of the polypeptides given in the specification, a method for identifying a compound useful in treating compulates its activity is useful for preparing a medicament for treating conjugates its activity is useful for preparing a medicament for treating conjugates its activity is useful for preparing a medicament for treating conjugates its activity is useful for preparing a medicament for treating conjugates its activity is useful for preparing a medicament for treating conjugates its activity is useful for preparing a medicament for treating conjugates its activity is useful for preparing a medicament for the sequence data for this patent did not form part of the printed conjudication, but was obtained in electronic form directly from WIPO at the specification, but was obtained in electronic form directly from WIPO at the polyment in the pain and part peduces.
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Gaps ; Score 191; DB 7; Length 585; Pred. No. 3.7e-13; 0; Mismatches 1; Indels 333 EREKEÇMMREKEELMLRLÖDYEEKTKKAERELSEÇIÇRALÇ 373 1 EREKEOMMREKEELMIRLODXEEKTKKAERELSEOIORALO 41 99.0%; 40; Conservative Local Similarity Sequence 585 AA; Query Match à

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AAY27443 standard; protein; 586 AA (first entry) 26-NOV-1999 AAY27443; RESULT 4 AAY27443

Pharmaceutical; ezrin; mutant; tumor; metastasis; human. Amino acid seguence of human ezrin polypeptide.

Homo sapiens

/note= "the Tyr at this position can be mutated (preferably to a Phe) to construct an ezrin mutant of the invention" Location/Qualifiers Misc-difference

Louvard D; Gautreau A, Crepaldi T, Arpin M,

INST CURIE.
CNRS CENT NAT RECH SCI 99WO-EP002054 98US-00040725 WPI; 1999-561851/47. WO9947150-A2 18-MAR-1999; 18-MAR-1998; 23-SEP-1999. (CURI-) CNRS ) 

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                                                                                    The invention provides a pharmaceutical composition containing ezrin protein, RNA or DNA mutated on tyrosine 353, or a functional fragment or derivative of the ezrin mutant. The new composition is useful for prevention and/or treatment of tumors, and especially metastasis. The present sequence represents the amino acid sequence of human ezrin (before the maturation by deletion of the first amino acid Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative disease; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 6q25.2-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention, the
               New composition for prevention and treatment of tumors and metastasis.
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                               99.0%; Score 191; DB 2; Length 586; 97.6%; Pred. No. 3.7e-13; tive 0; Mismatches 1; Indels
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Wang Z, W
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                                                                                                                                                                                                                                                                                                                        1 EREKEÇMMREKEELMLRLQDXEEKTKKAERELSEÇIQRALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human novel polypeptide sequence, SEQ ID NO:1711.
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7, Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 1711; 1185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC31629 standard; protein; 611 AA
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Wang D, Ma Y,
                                                   Example 1; Fig 1; 31pp; English.
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Zhou P, Ghosh M,
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                                                                                                                                                                                                                Sequence 586 AA;
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Matches
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Claim 20; Page 219; 765pp; English.

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recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; a method of detecting computation and acetodas of polymucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or methods of invention methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the invention; activity of the polymucleotide and/or polypeptides of the invention contig sequences corresponding to the cDNs sequences of the invention (ADC31861-ADC32627) and the polymucleotide and/or polypeptides of the invention contig sequences corresponding to the cDNs sequences of the invention (ADC31861-ADC32627) and the polympeptides encoded by the contigs (ADC32628 consetul in diagnostics, drug soreening, forensics, gene mapping, in the cuseful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other creating diseases such as Parkinson's disease, Alzheimer's also used for treating diseases such as Parkinson's disease, and in the recombinant producing many other types of diseases and other neurodegenerative diseases, and min the recombinant producing of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and in the recombinant producicon of a protein. The polypeptide sequence of the invention. Note: The sequence of the invention. Note: The sequence of the printed specification, but season the sequence of the printed specification, but seasons.
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ftp.wipo.int/pub/published_pct_sequences.
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Length 611; 1; Indels 334 EREKEÇMMEKEELMLRLQDYBEKTKKAERELSEÇIQRALQ 374 41 1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEQIORALO , Match
Local Similarity 97.6%; Pred. No. 3.9e-13; les 40; Conservative 0; Mismatches 1; Query Match Best Loc Matches δ

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Gaps

; 0

RESULT 6 AAU30004

(first entry) 18-DEC-2001

AAU30004;

AAU30004 standard; protein; 622

Novel human secreted protein #495

Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration, immune suppression, immune stimulation, anti-inflammatory, leukaemia.

Homo sapiens.

WO200179449-A2

25-OCT-2001

16-APR-2001; 2001WO-US008656

18-APR-2000; 2000US-00552929 26-JAN-2001; 2001US-00770160

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-611725/70.

Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.

New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

cancer.

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated at altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberran expression or physiological interactions of the polypeptide. Vectors comprising the considerable enough months to polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins of considerable ments. They may be used to increase stem cell proliferation, to regulate haematopoiesis, and in bone, cartilage, tendon and training as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human are also useful to invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
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Pred. No. 4e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 EREKEÇMMREKEELMLRIQDYEEKTKKAERELSEÇIQRALQ 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EREKEONMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human novel polypeptide sequence, SEQ ID NO:1713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC31631 standard; protein; 628 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 97.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-371981/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W02003029271-A2.
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Zhou P, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC31631;
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Matches
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The invention relates to 91 novel numen curva sequences (ADC2919-4) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel numen cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an entibody against a polypeptide of the invention is methods of invention in the complex of the invention; and methods of invention further discloses methods of peventing, tracting or numerical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the polynucleotide and/or monoclonal antibodies for carrying out the methods of the invention in the invention; methods for the polynucleotide and/or polypeptide of the invention are corresponding to the compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 conting sequences corresponding to the compounds that modulate the invention; methods for the polynucleotide and/or polypeptide; and 767 conting sequences corresponding to the confice of the invention are useful in diagnostics, dury screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other tratis, for assessing biodiversity, and animo acid sequences. They are also used for treating diseases such as Parkinson's glasses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders, wounds, burns, ulcers, osteoporosis, autolimmine diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective, vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; infectious disease; cardiovascular disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                       invention relates to 971 novel human cDNA sequences (ADC29919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease and other neurodegenerative diseases, anaemia, platelet
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Pred. No. 4e-13;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer antigen protein sequence SEQ ID NO:896.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EREKEOMMREKEELMIRLODXEEKTKKAERELSEQIQRALQ 41
                       Claim 20; SEQ ID NO 1713; 1185pp; English.
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Local Similarity 97.6%;
Les 40; Conservative 0
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Matches
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, wounds, renal disorders, reproductive disorders, immune system cardiovascular disorders, reproductive disorders, and cardiovascular disorders, infectious diseases, and cardiovascular disorders, AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                  Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 1449-1451; 2104pp; English.
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                                                                                                                                                                                                                                                                                                                                      antigens, useful for the treatm
disorders such as colon cancer.
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                                                                (HUMA-) HUMAN GENOME SCI INC.
12-MAR-1999; 99US-0124270P
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Best Local Similarity 97.6
Matches 40, Conservative
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                                                                                                                                    Ruben SM;
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D.
                                                                                                                                                                                                                                  N-PSDB; AAC98113
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Modified-site
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                                                                                                                                        Rosen CA,
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polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or
                                             Novel regulatory or unfolding peptides of ezrin that binds to
Hepreceptor, useful for inducing immune response for treating infectious
diseases and cancer.
                                                                                                                                                   The present sequence is domain B of human hepreceptor of human ezrin. The hepreceptor is a novel active site in human ezrin. Ezrin regulates the structure of the cortical cytoskeleron to control cell surface topography. The present invention relates to peptides (see AAB82041) that bind to hepreceptor with greater affinity than HEP1 (see AAB82046). The hepreceptor binding peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present sequence assembles into two anti-parallel helices with hepreceptor domain A (see AAB82019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acids encoding a range of human polypeptides, useful in genetic ion, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel human secreted polypeptides.
                                                                                                                                                                                                                                                                                                                                                                         80.8%; Score 156; DB 4; 97.1%; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MREKEELMIRLQDYEEKTKKAERELSEQIQRALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted protein #3551
                                                                                                                        Claim 5; Page 36; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU33060 standard; protein; 52
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26-JAN-2001; 2001US-00770160.
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Best Local Similarity 97.1;
Matches 33; Conservative
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               WPI; 2001-293287/31
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                                                                                                                                                                                                                                                                                                                                             Sequence 34 AA;
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AAU33060
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, delivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence subjected to pain, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a
physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUSSSIG AAUSSSIG AAUSSIG AAUSSIG AAUMAND AAUSPIG AAUMAND AAUMAND
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Best Local Similarity 78.4%; Pred. No. 2.2e-08; Matches 29; Conservative 3; Mismatches 5.
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                                                                                                                                                                                                                                                                                               secreted proteins of the invention
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 52 AA;
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Length 34; Indels

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compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypetides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating complete its activity is useful for preparing a medicament for treating in pain (e.g. spinal segmental nerve injury (NII)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification) but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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Pred. No. 3e-06;
9; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Protein P26038, SEQ ID NO 10541.
                                                                                                                                                                                                                                                                                                                                                                                     ADD45108 standard; protein; 576 AA
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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Best Local Similarity 63.4%;
Matches 26; Conservative
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                                                                                                                                                                                                                 Sequence 576 AA;
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that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound which regulates compound which regulates compound which regulates compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the polymetication, a method for identifying a compound useful in treating cartivity in an animal of one or more of the polypeptides given in the composition and a pharmaceutical composition comprising the one or more polymetication, a method for identifying a compound useful in treating cartivity is useful for preparing a medicament for more complete its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the sequence presented is a human proctein (shown in Table 2 of the sequence data for this patent did not form part of the printed contribution that was obtained in electronic form directly from WIPO at the contribution of the contribution of the printed cartivity is the contribution of the printed cartivity is the contribution of the contribut
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Best Local Similarity 63.4
Matches 26, Conservative
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The invention relates to a novel method for identifying a compound that modulates T lymphocyte activation. The method comprises contacting a T cell comprising an A-raf-1 or TCPTP/PTNZ polypeptide with a compound, where the A-raf-1 or TCPTP/PTNZ polypeptide is encoded by a nucleic acid that hybridises to a nucleic acid encoding a polypeptide having a sequence selected from two 606-amino acid sequence and a 415-amino acid sequence eslected from two 606-amino acid sequence and a 415-amino acid sequence selected from two 606-amino. The method of the invention has immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory activity. The method is useful for identifying compounds that modulate lymphocyte activation and migration, and for monitoring changes in cell surface marker expression, cytokine production, antibody production, con primary cells. The A-raf-1 or TCPPP/PTNZ proteins may be used as crivation and migration, e.g. for the treatment of diseases in which modulation of the immune response is desired such as delayed type compounds that suppress or activate lymphocyte activation and migration, e.g. for the treatment of diseases in which modulation of the immune response is desired such as delayed type confluence and chronic inflammation. Modulators of lymphocyte activation and acute and chronic inflammation. Modulators of lymphocyte activation and migration is asthma allergies, graft versus host disease, and acute and chronic inflammation. Modulators of lymphocyte activation and migration and disconders related T and B cell activation and inflammation. The present sequence is used in the exemplification of the
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Gaps .; Match 66.8%; Score 129; DB 6; Length 577; Local Similarity 63.4%; Pred. No. 3e-06; es 26; Conservative 9; Mismatches 6; Indels 1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEOIORALO 41 Sequence 577 AA; Query Match Best Loca Matches à

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Ā ADB70362 standard; protein; 577 RESULT 14 ADB70362 

Moesin SEQ ID NO:54. 04-DEC-2003

ADB70362;

cancer; malignant pleural mesothelioma; MPM; lung adenocarcinoma; squamous carcinoma; medulloblastoma; prostate cancer; breast cancer; diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer;

Homo sapiens.

WO2003021229-A2.

13-MAR-2003

05-SEP-2002; 2002WO-US028203

05-SEP-2001; 2001US-0317389P 30-AUG-2002; 2002US-00236031

(BGHM ) BRIGHAM & WOMENS HOSPITAL INC.

Bueno R; Gullans SR, Gordon GJ, Jensen RV,

WPI; 2003-290233/28. N-PSDB; ADB70361.

Diagnosing cancer cells in tissue sample, or determining prognosis or outcome of cancer patient, by calculating ratio of expression levels of genes that are differentially expressed in cancer and non cancer tissues.

New nucleic acid useful for diagnosing, preventing or treating diseases associated with aberrant vascular activity, angiogenesis, vasculogenesis and cartilage or bone formation, e.g. atherosclerosis or diabetes.

WPI; 2003-731500/69. N-PSDB; ADC77530, ADC77531.

The present invention describes an isolated nucleic acid (I) comprising:

Claim 25; SEQ ID NO 27; 70pp; English

Claim 77; Page 263-264; 396pp; English.

The present invention describes a method (M1) for diagnosing the presence

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the prognosis or non-cancer cells in a tissue sample, or determining the prognosis or outcome of a cancer patient. M1 involves providing a set of genes that are differentially expressed in cancerous or non-cancerous conditions, determining the expression levels of the set of genes and calculating a ratio of the expression levels of the differentially expressed genes. M1 is useful for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, where the cancer is malignant pleural mesotheliona (MPM), lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell prognosis or outcome of a cancer patient. The ratio of expression levels of differentially expressed genes is used as an indicator of cancer type, cancer class, and/or cancer prognosis, all of which are useful for determining a course of treatment of a patient. The present sequence represents a human protein which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hybridisation, testicular tumour differentially expressed gene 1, TDE1, patchy vessel, PTV, HLA class II region expressed gene 4, HKE4, vascular endothelial growth factor; VGGF, antirheumatic; antiarthritic; antiarteriosclerotic; antiabetic; ophthalmological; antipsoriatic; cytostatic; osteopathic; antiangiogenic; antisense gene therapy; aberrant vascular activity disorder; andiogenesis; vasculogenesis; carrilage formation disorder; bone formation disorder; rheumatoid arthritis; atherosclerosis; diabetes; retinopathies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wadman S, Essner J, Larson J, Clark KJ;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                          66.8%; Score 129; DB 7; Length 577; 63.4%; Pred. No. 3e-06; ive 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EREKEOMMREKEELMLRLQDXEEKTKKAERELSEQIORALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC77532 standard; protein; 577 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human moesin protein SEQ ID NO:27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  psoriasis; cancer; human; moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DISC-) DISCOVERY GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2003; 2003WO-US003747.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hackett PB, Nasevicius A,
Roberg-Perez S, Ekker SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 63.49
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                             Sequence 577 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-2004
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                                                                                                                                                                                                                                                                                             nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC77532;
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the problem of that hybridises under stringent conditions to a hybridisation probe comprising a sequence of 1422 (human (testicular) tumour differentially expressed gene I (TDEI) encoding CDNA ADC77521).

786 (human patchy vessels (FTV) encoding CDNA ADC77521) or 1410 (human patchy vessels (FTV) encoding CDNA ADC77531) base gairs (bp), or its complement; or (b) a sequence that is 90% identical to the probe sequences or their complements. Also described: (1) a composition comprising: (a) an isolated polypeptide comprising a sequence composition comprising: (a) an isolated polypeptide comprising a sequence composition comprising: (a) an isolated polypeptide comprising a sequence composition comprising: (b) a combination of a pharmaceutical captains and TDEI, PTV and HER4, or (b) a combination of a pharmaceutical carrier, vascular endothelial growth factor (VEGF) and TDEI or PTV; (2) an antisense polymucleic acid comprising a sequence, where the antisense polymucleic acid suppresses the expression of a human, mouse or zebrafish TDEI, PTV or HER4; and (3) a teleost comprising the antisense polymucleic acid suppresses the expression of a human, mouse or zebrafish TDEI, PTV or HER4; and (3) a teleost comprising the antisense polymucleic anticiabetic, ophthalmological, antisporiatic, cytostatic, osteopathic and antispotence acid (1) and polypeptide encoded by it, can be used for research, diagnostics, prophylaxis and therapeutic use. They may be used for research, diagnostics, prophylaxis and therapeutic use. They may be used for research, diagnostics, prophylaxis and therapeutic use. They may be used for research, diagnostics, prophylaxis wasculase associated with aberrant commutation. The diseases may include rheumatoid arthitis, at atherapeutic atherapeut invention.

The diseases may include rheumatoid arthitis or cancer. The atherasculase to a preventing or tethoresents returned by a career invention.
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Gaps .; 0 Query Match 66.8%; Score 129; DB 7; Length 577; Best Local Similarity 63.4%; Pred. No. 3e-06; Matches 26; Conservative 9; Mismatches 6; Indels

1 BREKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41

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Search completed: August 16, 2004, 09:43:46 Job time : 100 secs

334 EKEKEKIEREKEELMERLKQIEEQTKKAQQELEEQTRRALE 374

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us-09-856-070b-29.std.rag

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Appl Appli Appli

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APPLICANT: Institut Curie
APPLICANT: Crepaldi, Tiziana
APPLICANT: Gautreau, Alexis
APPLICANT: Louvard, Daniel
TITLE OF INVENTION: Parmaceutical composition containing ezrin mutated
TITLE OF INVENTION: Parmaceutical composition mutated
TITLE OF INVENTION: Parmaceutical composition containing ezrin mutated
TITLE OF INVENTION: OF 19900100
FILE REFERENCE: 391082000100
CURRENT FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 94, Application US/08056200
Fatent No. 5616500
Fatent No. 5616500
GENERAL INFORMATION:
APPLICANT: Lee, Sequence, Sequence, Sequence 94, Application Sequence, NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive, Sixteenth Floor CITY: Newport Beach
                                   Sequence
                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
                     Sequence
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Pred. No. 5.7e-14;
0; Mismatches 1; Indels
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US-09-154-750A-85
US-09-665-470A-12
US-09-592-06418-23
US-09-592-06418-23
US-08-875-4358-4
US-08-875-4358-4
US-09-759-359A-2
US-08-875-4358-3
US-08-875-4358-3
US-08-875-4358-3
US-08-830-349-4
US-08-630-349-5
US-08-630-349-5
US-08-630-349-6
US-08-630-349-6
US-08-630-349-6
US-08-630-349-6
US-08-630-349-6
US-08-630-349-6
US-08-630-349-6
US-08-630-349-6
US-08-630-349-6
US-08-630-34-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 97.6%;
Matches 40; Conservative
   TYPE: PRT
CORGANISM: Homo sapiens
US-09-040-725A-1
   US-09-040-725A-1
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LENGTH: 586
   RESULT 1
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Sequence 6436, Appl
Sequence 580, Appl
Sequence 573, Appl
Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
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                                                                                                                August 16, 2004, 09:45:46 , Search time 19 Seconds (without alignments) 111.403 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4
Sequence 1:
Sequence 1:
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                                                                                                                                                                                 US-09-856-070B-29
193
1 BREKEÇMMREKEBLMLRLQD......BEKTKKAERBLSEQIQRALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sued Patents AA:*
/cgn2_6/prodara/2/iaa/5A_COMB.pep:*
/cgn2_6/prodara/2/iaa/5B_COMB.pep;*
/cgn2_6/prodara/2/iaa/6A_COMB.pep;*
/cgn2_6/prodara/2/iaa/6B_COMB.pep;*
/cgn2_6/prodara/2/iaa/PCTUS_COMB.pep;*
/cgn2_6/prodara/2/iaa/PCTUS_COMB.pep;*
/cgn2_6/prodara/2/iaa/PCTUS_COMB.pep;*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-688-188B-15
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US-09-370-838-193
                                                                                                                                                                                                                                                                                                   389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
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Match
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Maximum DB seq
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Result Š. ö

Gaps

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GENERAL INC. 0003/LO.

GENERAL INC. 0003/LO.

APPLICANT GARY BRETON
TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
TITLE OF INVENTION: ULGENOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 682 BD NOS: 8344
LENGTH: 1180
                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                     37.8%; Score 73; DB 2; Length 1898; 41.2%; Pred. No. 3.2; tive 10; Mismatches 10; Indels
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APPLICANT: Young et al.
ITILE OF INFORMATION:
FILE REPERENCE: P2007P1
CURRENT PILITON DIMBER: U5/09/205,258
CURRENT PILITON NUMBER: U5/09/205,258
CURRENT PILITON DIMBER: U5/09/205,258
CURRENT PILITON DIMBER: U5/09/205,258
CURRENT PILITON DIMBER: U5/09/205,258
CURRENT PILITON DIMBER: U5/09/31/1422
EARLIER APPLICATION NUMBER: 00/046,885
EARLIER APPLICATION NUMBER: 06/049,375
EARLIER APPLICATION NUMBER: 06/049,375
EARLIER APPLICATION NUMBER: 06/049,375
EARLIER APPLICATION NUMBER: 06/049,375
EARLIER APPLICATION NUMBER: 06/049,881
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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1625 REBEQLLQEGEEQQLRRQERDRKFREBEQQLRRQ 1658
                                                                                                                                                                                                                                                                                                                      2 REKEÇMMREKEELMLRLQDXEEKTKKAERELSEQ 35
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Pred. No. 7;
9; Mismatches
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Sequence 6436, Application US/09543681A
Patent No. 6605709
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APPLICATION NUMBER: 60/048,880
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/048,896
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    TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1898 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-06-06
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(714) 760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                          Query Match
Best Local Similarity 41.2*
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                MOLECULE TYPE: protein US-08-800-644-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                        linear
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                                                                                                                  TYPE: amino
TOPOLOGY: li
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  TELEPHONE:
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US-09-205-258-580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Steinert, Peter M.
APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-In-Gyu
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
CORRESPONDENCES: 117
CORRESPONDENCES: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.8%; Score 73; DB 1; Length 1898; Best Local Similarity 41.2%; Pred. No. 3.2; Matches 14; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRAING SISIEM:
CURRANT APPLICATION DATA:
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,644
FILING DATE: 14-FEB-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fedick, Michael F.
REFERRACE/DOCKET NUMBER: 36,799
REFERRACE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/056,200
FILING DATE: 30-APR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 REKEOMMREKEELMLRLODXEEKTKKAERELSEQ 35
                                                                                                                                                                                                                                                                                                                                                         NIH054.001A
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 94, Application US/08800644
Patent No. 5958752
GENERAL INFORMATION:
APPLICANT: Steinert, Peter M.
                                                                                                                                                                                                                                                                              ATTORNEY/ACEDIT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1898 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1:--
CA
U.S.A.
                             COUNTRY: U
ZIP: 92660
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Query Natch 35 0; Score 675; DB 4; Length 64; Beel Local Similarity 39 54; Score 675; DB 4; Length 64; Beel Local Similarity 39 54; Score 675; DB 4; Length 64; Beel Local Similarity 39 54; Pred, Mo. 0. 38; Matches 15; Cocservative 10; Mismatches 10; Indels Db 15 ERAKERSKREGO--ERESOKERKZARRERNROLER 50

RESULT 6

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RESULT 7

RESULT 8

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HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
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34.2%; Score 66; DB 3; Length 764;
Best Local Similarity 44.4%; Pred. No. 7.4;
Matches 16; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 764; 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 OMMREKEELMLRLODXBEKTKKABRELSBOIGRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
FILING DATE:
PRIOR ADDATE:
                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 1
Pred. No. 7.4;
6; Mismatches
NAME: Fasse, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEFRAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09177431
Patent No. 6071700
GENERAL INFORMATION:
APPLICANT: He, Feng
APPLICANT: Jacobson, Allan S.
ITLE OF INVENTION: HETEROLOGOUS F.
ITLE OF INVENTION: ABSENCE OF NOW NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/955,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 0791.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.4%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/542-906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS: LENGTH: 764 amino acids
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amino acid
                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
STATE: MA
COUNTRY: USA
TE: 02110-2804
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US-09-177-431-4
                                                                                                                                                                                                                                                                                                                                                            US-08-375-300-4
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APPLICANT: Bacobson, Allan S.
APPLICANT: Bacobson, Allan S.
TITLE OF INVENTION: HETEROLOGGUS POLYPEPTIDE PRODUCTION IN
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED MENA DECAY FUNCTION
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
STREET: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (409)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-205-258-573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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35.0%; Score 67.5; DB 4; Length 567;
Best Local Similarity 39.5%; Pred. No. 3.7;
Matches 15; Conservative 10; Mismatches 10; Indels
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ZIP: 0210-2804

ZIP: 0210-2804

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,300

FILLNG DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 ERAKEREKRKEQ---EBEEGKEREKEAERERNROLER 504
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                                                                          EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER PEDLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER RELING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,978
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER PILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOCTWARE: PATENTIN VOMER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOCTWARE: PATENTIN VOMER: 2.0
             60/048,917
                                  FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08375300 Patent No. 5679566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: SITE
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US-08-375-300-4
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RESULT 11
US-09-177-431-2
Sequence 2, Application US/09177431
Patent No. 6071700
GENERAL INFORMATION:
APPLICANT: He, Feng
APPLICANT: Ho, Feng
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66; DB 1; Length 1089;
Pred. No. 11;
6; Mismatches 12; Indels
                                                                                                     COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,300
FILING DATE: 20-JAN.1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKetter
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FRASERQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 OMMREKEELMLRLODXEEKTKKAERELSEQIORALQ 41
                                                                                                                                                                                                                                                                     NAME: Fasse, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEPHONE: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07917/050001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/955,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REPERENCE/DOCKET NUMBER: 0791
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-9806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1089 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.4
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-375-300-2
                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200154
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                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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Patent No. 5679566

CENERAL INFORMATION:

APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.

TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED MENA DECAY FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66; DB 5; Length 764;
Pred. No. 7.4;
6; Mismatches 12; Indels
                                                                                                                                                 Sequence 4, Application PC/TUS9516930
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE
TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF
TITLE OF INVENTION: NONSENSE-MEDIATED mRNA DECAY.
TITLE OF INVENTION: FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLD FOC compatible
COMPUTER: Ploppy disk
COMPUTER: PLOPS MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 27-DEC-1995
PRIOR APPLICATION NUMBER: US 08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REGISTRATION NUMBER: 32,983
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 OMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
6 OMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
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225 Franklin Street Suite 3100
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SEQUENCE CHARACTERISTICS:
TYPE TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 44.4%;
Matches 16; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 764 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fis
STREET: 225 Fi
CITY: Boston
                                                                                                                 RESULT 9
PCT-US95-16930-4
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US-08-375-300-2
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Sequence 5, Application US/08257073 Patent No. 5766597 GENERAL INFORMATION:
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US-09-134-000C-6355
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                                                                                                                                       Score 66; DB 3; Length 1089;
Pred. No. 11;
6; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                              ADDRESSED : 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                    6 OMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PELLING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046WC
TELEPHONE: (617)542-5070
TELEFAX: (617)542-8906
                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application PC/TUS9516930 GENERAL INFORMATION:
                                                                                                                                         Query Match 34.2%;
Best Local Similarity 44.4%;
Matches 16; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAA.

TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
**TWOTH: 1089 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not relevant
                     SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
TYPE: amino acid
         INFORMATION FOR SEQ ID NO:
                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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STREET:
TTV: Bogton
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TOPOLOGY: lin
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                                                                                                           US-09-177-431-2
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RESULT 13 US-08-257-073-5

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Sequence 6355, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CITLE OF INVENTION:
CURRENT FILE REFERENCE:
CURRENT APPLICATION NUMBER:
CURRENT APPLICATION NUMBER:
CURRENT APPLICATION NUMBER:
CURRENT FILE 1997-08-13
PRIOR FILING DATE:
COSTON NUMBER:
C
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APPLICANT: Paoletti, Enzo
APPLICANT: de Taisne, Charles
APPLICANT: de Taisne, Charles
APPLICANT: de Taisne, Charles
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENE/ED/COCET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                   SEE: Curtis, Morris & Safford,
7: 530 Fifth Avenue, 25th Floor
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 09-UUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-UUN-1993
PRIOR APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-WAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .... US/08/257,073
09-JUN-1994
N: 424
                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (212) 840-0712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
33.9%; Score 65.5; DB 4; Length 818;
Best Local Similarity 39.0%; Pred. No. 9.1;
Matches 16; Conservative 10; Mismatches 4; Indels 1:
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CUUNTRY: U.S.A.
ZIP: 10.8.A.
ZUNITRY: U.S.A.
ZIP: 11.0.8.A.
ZIP: 10.8.A.
ZIP: 10.8.A.
ZIP: 10.8.A.
ZIP: 10.8.A.
ZIP: 10.8.A.
ZIP: 10.8.A.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: BC-DOS/MS-DOS
CURRENT APPLICATION DATA: BC-DOS/MS-DOS
TILING DATE:
CLASSIFICATION NUMBER: US/08/728,323A
ATYORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE CHARACTER: 121-278-0400
TELLEPAM: 212-278-0400
TELLEPAM: 212-391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: LIGS amino acids
TYPE: amino acids
TYPE: APPLICATION CONTRIBUTED ACIDS
TOTAL CONTRIBUTED ACIDS
TOTAL CONTRIBUTED ACIDS
TYPE: AMINO ACIDS
TYPE: AMINO ACIDS
TYPE: AMINO ACIDS
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46 ERQNLQQQKEELL-----BKKAKQAEQETVIERLKEQIQQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 EKEÇMMREKEELMLRLQDXEEKTKKAERE----LSEQIOR 38
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                                                                                                                                                                                          TYPE: PRT; ORGANISM: Enterococcus faecalis
US-09-134-000C-6355
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6355
LENGTH: 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
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MOLECULE TYPE: protein
US-08-728-323A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserva'
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STATE: New York
COUNTRY: U.S.A.
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US-08-728-323A-2
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Search completed: August 16, 2004, 09:46:37 Job time : 20 secs

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August 16, 2004, 09:49:27 ; Search time 46 Seconds (without alignments) 279.805 Million cell updates/sec
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1 EREKEQMMREKEELMLRLQD......EEKTKKAERELSEQIQRALQ
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| Canal Grant All Dubbaa (USO7 PUBCOMB.pep:*
| Canal Grant All Dubbaa (USO7 NEW PUB.pep:*
| Canal Grant All Dubbaa (USO6 NEW PUB.pep:*
| Canal Grant All Dubbaa (USO6 PUBCOMB.pep:*
| Canal Grant All Dubbaa (USO7 NEW PUB.pep:*
| Canal Grant All Dubbaa (USO7 NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-856-070B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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	_ ;	Sequence 4728	117,	2372,	1160	96	968	54,	27,	453	454	187	151	21,	24,	32544
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	Description	Sec	Sec	Sec	Sec	Sequence 896,	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec
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		80	7	372	160			**	7	23	4.5	7	_	_	***	544
		-47	-11,	A-2	A-1.	968	-89	B-5	4-2,	A-4	A-4	-18	-15	A-2	A-2	-32
SO,		698	275	765	765	-66	299	031	849	765	765	593	219	849	849	386
RIE	į	-90	16-	-80	08-	5-2	25-	36-	-09	-80	08-	48-	05-	-09	60-	29-
SUMMARIES		0-1	0-1	0-4	0-4	-92	9-6	0-2	0-3	0-4	0-4	9-0	-0-	0-3	.0-3	0-0
St	0	US-10-106-698-4728	US-10-116-275-117	US-10-408-765A-2372	US-10-408-765A-1160	JS-09-925-299-896	US-09-925-299-896	US-10-236-031B-54	US-10-360-849A-27	US-10-408-765A-453	JS-10-408-765A-454	US-10-648-593-187	US-10-205-219-15	US-10-360-849A-21	US-10-360-849A-24	US-10-029-386-32544
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	gth	436	586	586	630	635	635	577	577	577	577	577	583	579	579	213
	Match Length DB															
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* 5	Mat	56	9	9,	9	6	9	9	9	9	9	9	9	9	9	Ñ
	re	91	16	16	16	16	91	20	29	29	129	29	120	17	17	ī.
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4.6. 4.000 000 000 000 000 000 000 000 000	67.5
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## ALIGNMENTS

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Sequence 4726, Application US/10106698

publication No. US20030109690A1

GENERAL INFORMATION:

APPLICANT ON:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER:

CURRENT PLING DATE: 2002-03-27

PRIOR FILING DATE: 1090-09-28

PRIOR PLING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3.0

SEQ ID NO 4728

LING DATE: 1999-11-03

NUMBER: Patentin Ver. 3.0

SEQ ID NO 4728

LING DATE: 1999-11-03

NUMBER: Patentin Ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC_FEATURE
10.0CATION: (2)
0.THER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
1. NAME/KEY: MISC_FEATURE
1. LOCATION: (382)
1. CATION: (382)
2. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 40; Conserva
US-10-106-698-4728
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Gaps
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                                                                          APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Marnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 56008-465
CURRENT APPLICANTION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1160
LENGTH : 630
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Patent No US20020055627A1
GENERAL INCORMATION:
ITILE OF INVENTION:
FILE REPREMENTE: RAIO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: GY/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILLE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: DCT/US00/05883
PRIOR APPLICATION NUMBER: PCT/US00/05883
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Pred. No. 5.4e-12;
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Pred. No. 5.4e-12;
0; Mismatches 1;
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Best Local Similarity 97.6%;
Matches 40; Conservative 0
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Best Local Similarity 97.6%;
Matches 40; Conservative
                                              APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-896
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ORGANISM: Homo sapiens
GENERAL INFORMATION:
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US-09-925-299-896
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US-09-925-299-896
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LENGTH: 635
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                                                                                                                                            Sequence 117, Application US/10116275

| Publication No. US200302114761
| Publication No. US200302114761
| GENERAL INFORMATION:
| APPLICANT: Elan Pharmaceutical Technology
| APPLICANT: Brayden, David | Journal of APPLICANT: Brayden, David | Journal of APPLICANT: Brayden, David | Journal of APPLICANT: Brayden, David | APPLICANT: Higgins, Lisa | APPLICANT: Lisa |
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Pred. No. 5e-12;
0; Mismatches 1; Indels (
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Publication No. US20040101874A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ghosh, Sountra S.
APPLICANT: Ghosh, Sountra S.
APPLICANT: Talon, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glbson, Bradford W.
APPLICANT: Glbson, Taylor W.
APPLICA
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CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SQTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2372
LENGTH: 586
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Best Local Similarity 97.6%;
Matches 40; Conservative
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US-10-116-275-117
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ORGANISM: Homo sapiens
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US-10-408-765A-2372
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US-10-408-765A-1160
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Pahy, Edin D.
APPLICANT: Tang, Bing
APPLICANT: Glang, Bradford W.
APPLICANT: Glann, Gary M.
APPLICANT: Glann, Gary M.
APPLICANT: Warnock, Dale E.
AITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILLS REPERENDE: 660088 465
CURRENT APPLICATION NYMER: US/10/408,765A
CURRENT FILLNG DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 577
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APPLICANT: Gary
APPLICANT: Taylor, Stradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 1DENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 2003-04-04
TITLE OF INVENTION: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: Falled DAIE: And Mindows Version 4.0
SEQ ID NO 454
LENGTH: 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 453, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.2
SEQ ID NO 27
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Best Local Similarity 63.43
Matches 26; Conservative
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ORGANISM: Homo sapiens
US-10-408-765A-453
                                                                                                             LENGTH: 577
TYPE: PRT
CRGANISM: homo sapiens
US-10-360-849A-27
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Publication No. US2003022249A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hackett, Perry
APPLICANT: Besner, Jeffrey
APPLICANT: Larson, Joh
APPLICANT: Larson, Joh
APPLICANT: Roberg-Perez, Sharon
APPLICANT: Nadman, Sharon
APPLICANT: Wadman, Sharon
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                                                                                                                                                                                                                                                                             Score 191; DB 10; Length 635;
Pred. No. 5.4e-12;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                1 EREKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 54, Application US/10236031B
Publication No. US20030219760A1
GENERAL INFORMATION:
APPLICANT: Gullans, Steven R.
APPLICANT: GULLANS BO801/70265 (JRV/JAV)
CURRENT APPLICATION NUMBER: US/10/236,031B
CURRENT FILING DATE: 2002-09-05
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66.8%; Score 129; DB 15;
Best Local Similarity 63.4%; Pred. No. 1.5e-05;
Matches 26; Conservative 9; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/317,389
PRIOR FILING DATE: 2001-09-05
PRIOR PELICATION NUMBER: US 60/407,431
WINDER PLICATION STATE 102
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/354,978
PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1556 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 896 LENGTH: 635
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.6%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US-10-360-849A-27
                                                                                                                                                                                                                              US-09-925-299-896
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US-10-236-031B-54
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SEQ ID NO 54
LENGTH: 577
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334 EXEKERIEREKEELMERLRQIEEQIVKAQKELEEQTRKALE 374
1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEQIQRALQ
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                                                                                                                                                                                                                                            ; Sequence 21, Application US/10360849A; publication No. US20030220249A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Discovery Genomics, Inc. APPLICANT: Hackett, Perry
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Discovery Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                         Hackett, Perry
Nasevicius, Aidas
Esener, Jeffrey
Clark, Karl
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SOFTWARE: PatentIn version 3.2
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Best Local Similarity 56.1<sup>3</sup>
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: danio rerio
US-10-360-849A-21
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US-10-360-849A-21
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LENGTH: 579
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Publication No. US20040106132A1
GENERAL INFORMATION:
Papelication No. US20040106132A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
INTILE OF INVENTION:
PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273 NP
CURRENT APPLICATION NUMBER: US/10/648,593
CURRENT PILIOS DATE: 2003-08-26
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR RILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE PATENTIN Version 3.2
SEQ ID NO 187
LENGTH: 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQUENCE 151, Application US/10205219
| Sequence 151, Application US/10205219
| Publication No. US2030138803A1
| GENERAL INFORMATION:
| APPLICANT: Warner-Lambert Company
| APPLICANT: Dixon, Alistair
| APPLICANT: Pinnock, Robert
| APPLICANT: Pinnock, Robert
| APPLICANT: Pinnock, Robert
| APPLICANT: Pinnock, Robert
| APPLICANT: Dixon, Alistair
| CURRENT APPLICATION NUMBER: US/10/205,219
| CURRENT APPLICATION NUMBER: GB 0118354.0
| PRIOR PILING DATE: 2001-07-27
| NUMBER OF SEQ ID NOS: 197
| SEQ ID NO 151
| LENGTH: DIX APPLICATION OF TAXABLE APPLICATION
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                                                                                                              Query Match 66.8%; Score 129; DB 16; Length 577; Best Local Similarity 63.4%; Pred. No. 1.5e-05; Matches 26; Conservative 9; Mismatches 6; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 EKEKEKIEREKEELMERLKQIEEQTKKAQQELEEQTRRALE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EREKEOMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                               1 EREKEOMMREKEELMLRLQDXEEKTKKAERELSEQIORALQ 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-648-593-187
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           ; ORGANISM: Homo sapiens
US-10-408-765A-454
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APPLICANT: Essner, Jeffrey
APPLICANT: Clark, Karl
APPLICANT: Clark, Karl
APPLICANT: Clark, Karl
APPLICANT: Larson, Jon
APPLICANT: Larson, Jon
APPLICANT: Roberg-Perez, Sharon
APPLICANT: Roberg-Perez, Sharon
APPLICANT: Roberg-Perez, Sharon
APPLICANT: Madman, Shanton
TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/10/360,849A
CURRENT APPLICATION NUMBER: US 60/354,978
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 21
LENGTH: SA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hackett, Perry
APPLICANT: Hackett, Perry
APPLICANT: Besner, Jeffrey
APPLICANT: Besner, Jeffrey
APPLICANT: Clark, Karl
APPLICANT: Clark, Karl
APPLICANT: Larson, Jon
APPLICANT: Area
APPLICANT: Madman, Stephen
APPLICANT: Wadman, Sharnon
TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORWATION,
TITLE OF INVENTION: BONB FORWATION, AND WETHODS OF USE THEREOF
FILE REFREENCE: 3021.05U30
CURRENT APPLICATION NUMBER: US/10/360,849A
CURRENT PILING DATE: 2003-02-07
PRIOR FILING DATE: 2003-02-07
WINDER OF FILE MEDIAL CALLON NUMBER: US 60/354,978
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Sequence 3244

Sequence 32424

Sequence 32424

Sequence 32428

Sequence 32428

Sequence 32428

Sequence 32428

Sequence 32428

Sequence 32428

Sequence 32544
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Query Match 60.6%; Score 117; DB 15; Length 579; Best Local Similarity 56.1%; Pred. No. 0.00026; Matches 23; Conservative 12; Mismatches 6; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYPE: PRT
CORGANISM: Homo sapiens
CORGANISM: Homo sapiens
FEATURE:
COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.1
COTHER INFORMATION: SWISSPROT HIT: P26038, EVALUE 2.00e-97
US-10-029-386-32544
                                                                                                              1 EREKEOMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
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US-10-029-386-32544
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Mon Aug 16 10:46:53 2004

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ezrin [validated]
hypothetical prote
ezrin - bovine
ezrin - bovine
moesin - human
moesin - pig
radixin - pig
radixin - mouse
radixin - human
trichohyalin - rab
plectin - human
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KIAA6642 protein -
translation initia
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class II INCENP pro
hypothetical prote
heat shock protein
hypothetical prote
unknown protein, 7
101K malaria antig
hypothetical prote
protein F53H1.4 [i
hypothetical prote
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1 EREKEGMMREKEELMLRLQD......EEKTKKAERELSEQIQRALQ 41
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                   283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                               - protein search, using sw model
                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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T119756
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T1663038
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Maximum DB seq length: 2000000000
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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T00365	T21379	E70318	833068	T15087	A59287	T07210	F75216	S48244	A54803	T00263	JC5837	T13564	T28184	T00367	T21048
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35.0	34.7	34.5	34.5	34.5	34.5	34.2	34.2	34.2	34.2	34.2	34.2	34.2	33.9	33.9	33.9
67.5	67	66.5	66.5	66.5	66.5	99	99	99	99	99	99	99	65.5	65.5	65.5
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## ALIGNMENTS

	RESULT 1 A34400 ezrin (validated) - human Nighternate names: cytovillin; p81 protein; villin 2 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 22-Jun-1990 #sequence revision 14-Jul-1994 #text_change 24-Nov-2003 C;Accession: A34400; S02263; E61002 R;Yurunen, O.; Winqvist, R.; Pakkanen, R.; Grzeschik, K.H.; Wahlstroem, T.; Vaheri, A. J. Biol. Chem. 264, 16727-16732, 1989 A;Title: Cytovillin, a microvillar M-r 75,000 protein. cDNA sequence, prokaryotic express
	A;Reference number: A34400; MUID:89380299; PMID:2674140 A;Accession: A34400 A;Accession: A34400 A;Molecule type: mRNA A;Residues: 1-586 <tur> A;Cross-references: GB:005021 A;Note: the translation of residues 1-11 is not given A;Note: parts of this sequence were confirmed by protein sequencing R;Gould, K.L.; Bretscher, A.; Esch, F.S.; Hunter, T. R;Gould, K.L.; Sretscher, A.; Esch, F.S.; Hunter, T. B;Mould, K.L.; And Cloning and sequencing of the protein-tyrosine kinase substrate, ezrin, rev. A;Reference number: S09263; MUID:90076135; PMID:2591371</tur>
	A;Molecule type: mRNA A;Molecule type: 2-586 <gou> A;Cross-references: GB:X51521; NID:g31282; PIDN:CAA35893.1; PID:g31283 A;Cross-references: GB:X51521; NID:g31282; PIDN:CAA35893.1; PID:g31283 B;Bauw, G:; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; Ce B;Bauw, G:; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; Ce A;Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencing A;Reference number: A61002; MUID:91031404; PMID:1699755</gou>
·	A;Nolectule type: protein A;Nolectule type: protein A;Note: it is not certain whether this material represents ezrin or radixin (see entry A; A;Note: this material corresponds to transformed epithelial amnion cell (AMA) database p; C;Comment: This protein is located in microvilli and is proposed to play a role in modula C;Genetics: A;Gene: GDB:VIL2 A;Gross-references: GDB:120489; OMIM:123900
	C;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology C;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-associated protein; phosphoprotein F;2-586/product: ezrin #status experimental <pre></pre> F;2-586/product: ezrin #status experimental <pre></pre> F;7-291/Domain: protein 4.1 membrane-binding domain homology <b41> F;553-586/Region: actin binding #status predicted F;653-586/Region: actin binding #status predicted F;66/Binding site: phosphate (Ser) (covalent) #status predicted F;214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted</b41>
	Query Match Best Local Similarity 97.6%; Pred. No. 5.9e-11; Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 EREKEÇMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41

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Accession: T47177

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R.Egerton, M.; Burgess, W.H.; Chen, D.; Druker, B.J.; Bretscher, A.; Samelson, L.E.
V. Immunol. 149, 1847-1852, 1992
A.Title: Identification of earin as an 81-kDa tyrosine-phosphorylated protein in T cells.
A.Reference number: A46501; MUID:92388649; PMID:1381389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. Experimental source: MEL lpr/lpr, T-cells
A.Note: sequence extracted from NCBI backbone (NCBIP:112940)
C. Comment: This protein is located in microvilli and is proposed to play a role in modula C. Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology C. Keywords: actin binding; cytoskeleton; cytoskeleton; protein 4.1 membrane-associated protein; phosphoprom F;2-586/Product: ezrin #status predicted cMAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-577 <1.AN>
A;Cross-references: GB:M69066; NID:g188625; PIDN:AAA36322.1; PID:g188626
C;Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasma me
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/Gene: GDB.MSN
A/Cross-references: GDB:116819; OMIM:309845
A/Cross-references: GDB:116819; OMIM:309845
A/Cross-references: GDB:116819; OMIM:309845
C;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology
C;Keywords: actin binding; cytoskeleton; membrane protein
F;2-577/Product: moesin #stetus predicted <MATP-
F;7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
F;544-577/Region: actin binding #status predicted
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Porc, Natl. Acad. Sci. U.S.A. 88, 8297-8301, 1991
A;Title: Moesin: a member of the protein 4.1-talin-ezrin family of proteins.
A;Reference number: A41289; MUID:92020840; PMID:1924289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N/Alternate names: membrane-organizing extension spike protein
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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F;553-586/Region: actin binding #status predicted
F;66/Binding site: phosphate (Ser) (covalent) #status predicted
F;214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted
A;Cross-references: EMBL:X60671; NID:g50880; PIDN:CAA43086.1; PID:g50881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Mesidues: 27-33, "2 < KEG2>
A;Essidues: 27-33, "2 < KEG2>
A;Experimental source: MRL lpr/lpr, T-cells
A;Note: sequence extracted from NCBI backbone (NCBIP:112936)
                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Molecule type: protein
A,Residues: 412-426 - EGB2
A,Experimental source: MRL lpr/lpr, T-cells
A,Nore: sequence extracted from NCBI backbone (NCBIP:112938)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: protein
A, Residues: 53-57,148, 'L',150,'G',152-155 < EG3>
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                                                                                                                                                                                                                                                        A; Accession: C46501
A; Status: preliminary
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R;Lankes, W.T.; Furt
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: 15-0ct-1996 #sequence_revision 15-0ct-1996 #text_change 24-Nov-2003
C;Accession. 145889
R;Bergson, C.M.; Zhao, H.; Saijoh, K.; Duman, R.S.; Nestler, E.J.
R;Bergson, C.M.; Zhao, H.; Saijoh, K.; Duman, R.S.; Nestler, E.J.
A;Hergson, C.M.; Zhao, H.; Saijoh, K.; Duman, R.S.; Nestler, E.J.
A;Hergson, C.M.; Zhao, H.; Saijoh, K.; Duman, R.S.; Nestler, E.J.
A;Hergson, C.M.; Zhao, H.; Saijoh, K.; Duman, R.S.; Nestler, E.J.
A;Hergerence number: 145889
A;Accession: 145889
A;Access
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C;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology
F;7-291/Domain: protein 4.1 membrane-binding domain homology <841>
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                                                                                                                                                                                                                                                                                                                                                                                                    Cidate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 24-Nov-2003 CiAccession: T47177
R;Ottenwarelder, B:, Obermaier, B.; Mewes, H.W.; Weil, B.; Wiemann, S. aubmitted to the Prorein Sequence Database, March 2000
A;Reference number: Z24377
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: B41129; C46501; A46501; B46501; S24200
R;Funayama, N.; Magafuchi, A.; Sato, N.; Tsukita, S.; Tsukita, S.
A;Title: Radixin is a novel member of the band 4.1 family.
A;Reference number: A41129; MUID:92064635; PMID:1955455
A;Accession: B41129
A;Reference number: A61129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-630 <AAAA
A;Cross-references: EMBL.Ai162086
A;Experimental source: adult melanoma (MeWo cell line); clone DKFZp762H157
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Best Local Similarity 97.6%; Pred. No. 6.3e-11;
Dest Local Similarity 97.6%; Pred. No. 6.3e-11; Indels
334 BREKEQMMREKEELMLRLQDYEEKTKKABRELSEQIQRALQ 374
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                                                                                                                                                                                                                                                                                                              hypothetical protein DKFZp762H157.1 - human (fragment)
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                                                                                                                                                                                                                                                                                                                                                                    Species: Homo sapiens (man)
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Matches 36; Conserv
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Query Match

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C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
C;Accession: A46127
R;Wilgenbus, K.K.; Milatovich, A.; Francke, U.; Furthmayr, H.
R;Wilgenbus, E.K.; Milatovich, A.; Francke, U.; Furthmayr, H.
A;Title: Molecular cloning, cDNA sequence, and chromosomal assignment of the human radixi
A;Reference number: A46127; MUID:93252378; PMID:8486357
                           A,Accession: A41129
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: FTUN-
A,Molecule type: FTUN-
A,Molecule type: TFUN-
C,Superfamily: exin/radixin/moesin for the barbed end of actin filaments and it is I
C,Superfamily: exin/radixin/moesin family; protein 4.1 membrane-binding domain homology
C,Reywords: actin binding typeseleton
F,470-477/Region: protein 4.1 membrane-binding domain homology <B41>
F,550-583/Region: actin binding #status predicted
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A;Residues: 1-1407 <PIE>
A;Cross-references: EMBL:Z19092; NID:g1746; PIDN:CAA79519.1; PID:g1747
C;Comment: Trichohyalin is a protein of the medulla of the hair and of the inner root she covalent modifications to this protein include conversion of arginine to citrulline and t
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S.Superfamily: estin/raddxin/moesin family; protein 4.1 membrane-binding domain homology
C;Keywords: actin binding; cytoskeleton
F;7-291/Domain: protein 4.1 membrane-binding domain homology <841>
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A;Note: sequence extracted from NCBI backbone (NCBIN:131481, NCBIP:131482)
C;Comment: Radixin is a capping protein for the barbed end of actin filaments and it
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Bate: 12-Mar-1993 #sequence_revision 01_Mar-1996 #text_change 22-Jun-1999
C;Accession: 828598
R;Fietz, M.J.; Rogers, G.E.
submitted to the EMBL Data Library, December 1992
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A;Description: Examination of the gene encoding rabbit trichohyalin.
A;Reference number: S28589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 EKEKERIEREKEBIMERIRQIEEQTVKAQKELEEQTRKALE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EREKEOMMREKEELMLRLQDXEEKTKKAERELSEGIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EREKEOMMREKEELMLRLODXEEKTKKAERELSEOIORALO 41
A; Reference number: A41129; MUID: 92064635; PMID: 1955455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.7%; Score 119; DB 1; Lv
58.5%; Pred. No. 0.00036;
tive 10; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.2%; Score 120; DB 1; 58.5%; Pred. No. 0.00029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;470-477/Region: proline-rich
F;550-583/Region: actin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:136270; OMIM:179410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-583 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S28589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A46127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             radixin - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Gene: GDB: RDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                    Messur as membrane-organizing extension spike protein moesin page 199804

N.Alternate names: membrane-organizing extension spike protein c) Species: Sus scrofa domestica (domestic pig)
C; Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
C; Accession: 839804
R; Lankes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.
B; Chankes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.
R; Lankes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.
R; Reference number: 839804; MUID:94092743; PMID:8268231
A; Tile: Cloning and sequencing of porcine moesin and radixin cDNA and identification of A; Reference number: 839804; MUID:94092743; PMID:8268231
A; Residues: 1-577 ~LAN
A; Residues: 1-577 ~LAN
A; Residues: 1-577 ~LAN
A; Residues: 1-577 ~LAN
C; Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology
C; Keywords: actin binding: vroiseleteron; membrane protein
F; 2-577/Product: moesin #status predicted AMAT>
F; 2-577/Product: moesin #status predicted
F; 5-44-577/Region: actin binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S39805
radaxin - pig
radaxin - pig
cybere: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
C;Dete: 19-May-1994 #sequence_revision 17-482, 1993
R;Lankes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.
Biochim. Biophys. Acta 1216, 479-482, 1993
A;Tele: 10-Ining and sequencing of porcine moesin and radixin cDNA and identification of A;Reference number: S39804, MUID:94092743; PMID:8268231
A;Accession: S39805
A;Accession: S39805
A;Accession: S39805
A;Accession: S39805
C;Comment: Radixin is a capping protein for the barbed end of actin filaments and it is C;Comment: Radixin is a capping protein for the barbed end of actin filaments and it is C;Comment: Radixin is a capping protein for the barbed end of actin filaments and it is C;Comment: Radixin is a capping protein for the barbed end of actin filaments and it is C;Comment: Radixin is confine-rich
F;77-291/Domain: protein 4.1 membrane-binding domain homology <841>
F;50-583/Region: proline-rich
F;550-583/Region: actin binding #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 03-Mus 1992 #sequence_revision 14-Jul-1994 #text_change 24-Nov-2003
C;Accession: A41129; S24201
R;Funayama, N.; Nagafuchi, A.; Satco, N.; Tsukita, S.; Tsukita, S.
A;Title: Radixin is a novel member of the band 4.1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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65.0%; Pred. No. 6.3e-05;
ive 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.7%; Score 121; DB 1; Length 583; 58.5%; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
334 EKEKEKIEREKEELMERLKQIBEQTKKAQQELEEQTRRALE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 EKEKERIEREKEELMERLRQIEEQTMKAQKELBEGTRKALE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 EKEKEKIEREKEELMERLKQIEEQTKKAQQELEEQTRRAL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEGIORALO 41
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26; Conservative
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hes 24; Conservative
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homology <EF2>

1005 REBEQLLQEREEERLRRQERDRKFREEERQLRRQ 1038 2 REKEQMMREKEELMLRLQDXEEKTKKAERELSEQ

RESULT 11 G02520

Local Similarity les 15; Conserv

Query Match Best Local S: Matches 15

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1898 <-LEE>
A; Residues: 1-1898 <-LEE>
A; Cross-references: GB: LD9190; NID: 9292835; PIDN: AAA65582.1; PID: 9292836
A; Note: authors translated the codon AGG for residue 1714 as Pro
C; Comment: Trichbhyalin is a protein of the medulla of the hair and of the inner root she
Covalent modifications to this protein include conversion of arginine to citrulline and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable seryl-tRNA synthetase APE1976 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix.
C;Species: Aeropyrum pernix.
C;Date: Abug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: B72500
C;Accession: B72500
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki, J.; Kn DNA Res. G, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyra, A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72500
A;Accession: B7250
A;Residues: Dreliminary
A;Molecule type: DNA
A;Residues: 1-463 «KAM»
A;Residues: 1-464 «KAM»
A;Residues: 1-464 «KAM»
A;Residues: 1-464 «KAM»
A;Residues: 1-464 «KAM»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                       Gaps
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C,Superfamily: trichohyalin; calmodulin repeat homology
C,Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
F,49-81/Domain: calmodulin repeat homology <EF2>
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0
                                                                                                                                                                           Query Match 38.9%; Score 75; DB 1; Length 1549; Best Local Similarity 40.5%; Pred. No. 13; Matches 17; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 37.8%; Score 73; DB 1; Length 1898; Local Similarity 41.2%; Pred. No. 24; es 14; Conservative 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.3%; Score 72; DB 2; Length 463; Best Local Similarity 41.2%; Pred. No. 7.8; Matches 14; Conservative 8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              3 EKEQMMREKEELMLRLQD-----XEEKTKKAERELSEQIQR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ed (cross-linking) protein.
A;Reference number: A45973; MUID:93280194; PMID:7685034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 REKEQMMREKEELMLRLQDXEEKTKKAERELSEQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:136223; OMIM:190370
    F,49-81/Domain: calmodulin repeat home F;387-851/Region: 28-residue repeats F;886-1519/Region: 23-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serine-tRNA ligase
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C;Gentcics:
A;Gene: AB1976
C;Superfamily: serine-tRNA ligas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trichohyalin - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: THH
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C:Species: Ovis crientalis aries, Ovis ammon aries (domestic sheep)
C:Species: Ovis crientalis aries, Ovis ammon aries (domestic sheep)
C:Accession: A40691; A34209; S32633
R:Fietz, M. J: McLauchlan, C.J.; Campbell, M.T.; Rogers, G.E.
A/Title: Analysis of the sheep trichohyalin gene: potential structural and calcium-bindi
A;Reference numbers. A40691; MUID:9326018; PMID:7684041
A;Accession: A40691
A;Accession: A40691
A;Molecule type: DNA
A;Residues: 1-1549 cFIE>
A;Cross-references: EMEL:218361; NID:225540; PIDN:CAA79165.1; PID:9255941
A;Molecule type: DNA
A;Cross-references: EMEL:218361; NID:9295940; PIDN:CAA79165.1; PID:9295941
A;Note: sequence extracted from NCBI backbone (NCBIP:132511)
A;Note: sequence extracted from NCBI backbone (NCBIP:132511)
A;Note: sequence extracted from NCBI backbone (NCBIP:132511)
A;Note: sequence extracted amino acid sequence for trichohyalin, a differentiation marker
A;Accession: A34209
A;Accession: A34209
A;Accession: A34209
A;Accession: A34209
A;Accession: A34209
A;Accession: A34209
A;Accession: A1200-1151,1205-1257,1281-1398,'G',1400-1549 cFI2>
A;Cross-references: GB:X55695; NID:91827; PID:91828
C;Comment: Trichohyalin is a protein include conversion of arginine to citrulline and C;Ganetics:
A;Introns: 46/3
A;Note: single copy gene
C;Superfamily: trichohyalin; calmodulin repeat homology
C;Superfamily: trichohyalin; calmodulin repeat homology
C;Keywords: calcium binding; citrulline; EF hand; hair; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein;68-283/Domain: alpha-actinin actin-binding domain homology <ACT>
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C;Genetics:
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: G0220
R;McLean, W.H.I.; Smith, F.J.D.
Submitted to the EMBL Data Library, March 1996
A;Reference number: H01385
A;Accession: G02520
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4574 cMCL>
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C;Genetics:
A;Introns: 46/3
C;Superfamily: trichohyalin; calmodulin repeat homology
C;Superfamily: trichohyalin; calmodulin repeat hand; hair; tandem repeat
F;49-81/Domain: calmodulin repeat homology <EF2>
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                                                                                                                                                                                                                                                              40.9%; Score 79; DB 1; Length 1407; llarity 44.1%; Pred. No. 4.9; Conservative 10; Mismatches 9; Indels
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REKEGMMREKEELMLRLQDXEEKTKKAERELSEGIGRALO

à d RESULT 12 A40691

A,Gene: PLEC1 C,Superfamily: F,68-283/Domair

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EKEOMMREKEELMLRLODXEEKTKKAERELSEQI 36

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plectin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accesion: A39638; S21876
C;Accesion: A39638; Luber, K.; Weitzer, G.; Castanon, M.J.; Hauptmann, R.; Stratowa J. Cell Biol. 114, 83-99, 1991
A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with A;Reference number: A39638, MUD:91268156; PMID:2050743
A;Accession: A39638
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4687 - WIC>
A;Acsos-references: EMBL:X59601; NID:g1292885; PIDN:CAA42169.1; PID:g1561642
C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S;6-10370pmain: alpha-actinin actin-binding domain homology cACT>
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37.0%; Score 71.5; DB 1; Length 4687;

Best Local Similarity 31.8%; Pred. No. 78;

Matches 14; Conservative 15; Mismatches 12; Indels 3;
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Q9yaga aeropyrum p
P37109 orycrolus
P27709 homo sapien
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1 BREKEQMMREKEELMLRLQD......BEKTKKAERELSEQIQRALQ
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                   "Identification of ezrin as an 81-kDa tyrosine-phosphorylated protein
                                                                                                                                                                                                                                                                                  -!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
                                           Egerton M., Moritz R.L., Druker B., Kelso A., Simpson R.J., and "Identification of the 70kD heat shock cognate protein (Hsc70) and alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
                                                                                                  [6]
PHOSPHORYLATION BY PDGFR.
PHOSPHORYLATION BY PDGFR.
MEDLINE=92406868; PubMed=1382070;
Krieg J., Hunter T.;
"Identification of the two major epidermal growth factor-induced tyrosine phosphorylation sites in the microvillar core protein arrin.";
                                                                                                                                                                                                                                                                                                                          (cytoplasmic side).
--- TISSUE SPECIFICITY: Component of the microvilli of intestinal epithelial cells.
--- PTM: Phosphorylated by tyrosine-protein kinases.
--- SIMILARITY: Contains I FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50057; PERM_3; 1.
Structural protein; Cytoskeleton; Phosphorylation; Polymorphism;
                                                                                                                                                                                                                 MEDLINE-92388649; PubMed=1381389;
Egerton M., Burgess W.H., Chen D., Druker B.J., Bretscher A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 585;
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2A844D140E3B06CC CRC64;
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                         ochem. Biophys. Res. Commun. 224:666-674(1996).
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Pred. No. 1.1e-10;
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EMBL; J05021; AAAC1278.1; ALT_INIT.
EMBL; AL162086; CAB82418.1; ALT_INIT.
EMBL; BC013903; AAH13903.1; -:
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InterPro: IPR000299; Band 4.1.
InterPro: IPR000799; Estrad/moesin.
Pfam; PF0013; Band 41, 1.
Pfam; PF00169; ERM; 1.
PRINTS; PR00195; BAND41.
SMART; SM00295; BAND41.
PROSITE; PS00660; FERM 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS00661; FERM 2; 1.
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                      SEQUENCE OF 171-179 AND 342-349.
MEDLINE=96311348; PubMed=8713105;
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J. Immunol. 149:1847-1852(1992)
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PDB; INIZ; 25-FEB-03.
SWISS-2DPAGE; P15311; HUMAN.
Genew; HCNC:12691; VIL2.
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Best Local Similarity

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-96239137; PubMed-8660651;
Galat A., Gerbod M.C., Bouet F., Riviere S.;
"Proteins and their amino acid compositions: uniqueness, variability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and applications.";
Arch. Biochem. Biophys. 330:229-237(1996).
-!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-!- SUBCELLULAR LOCATION: Microvillar peripheral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bergson C.M., Zhao H., Saijoh K., Duman R.S., Nestler E.J.; Bergson C.M., Eazin and osteonectin, two proteins associated with cell shape and growth, are enriched in the locus coeruleus."; Mol. Cell. Neurosci. 4:64-73(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                      333 EREKEÇMMREKEELMLRLÇDYEEKTKKAERELSEÇIÇRALÇ 373
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-!- PTM: Phosphorylated by tyrosine-protein kinases.
-!- SIMILARITY: Contains 1 FERM domain.
1 EREKEQMWREKEELMLRLQDXEEKTKKAERELSEQIQRALQ
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                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.2%; Score 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M98498; AAA30510.1; --
PTR; 145889; 145889.
Interpro; IPR000299; Barad 4.1.
Interpro; IPR000998; E2/rad/moesin.
Interpro; IPR008954; Moesin.
Pfam; PP00373; Band 41; 1.
Pfam; PP00769; ERM; 1.
PRINTS; PR00935; BAND41.
SNART; SM00295; B41; 1.
PROSITE; PS00660; PERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS00661; FERM 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68629 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-15 AND 126-140.
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294
145
                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            580, AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structural print MET
                                                                                                                                                                                                           EZRI BOVIN
P31976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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MOD_RES
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324
569
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Q8HZQ5;
10-OCT-2003 (
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Best Local
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SOLUTION OF THE PROPERTY OF TH
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SEQUENCE FROM N.A.

MACAZAKI Y., FURTHON M., SASHWAWA T., Adachi J., Bono H., Kondo S.,

NIKAIGO I., OBATO N., SAITO R., SUZUKI H., YAMMANA I., KIYOBAWA H.,

NIKAIGO I., OBATO N., SAITO R., SUZUKI H., YAMMANA I., KIYOBAWA H.,

RADALI E., TOMATU Y., HASCAGAW Y., NOGAMI A., SCHONDSCH C., GOJOBORI T.,

BAIAKE J.A., BRAGH D., BRINSIC V., CHOKINIA C., COTADAI L.E., COUSINS S.,

BAIAKE J.A., BRAGH D., BRINSIC V., CHOKINIA C., COTADAI L.E., COUSINS S.,

AND DAILA E., Dragani T.A., Fletcher C.F., FORTEST A., GOUGH J.,

RAMAGIOTE N., MALDIAI N., Lee Y., Lenhard B., Lyons P.A.,

KANAJI H., KAWASAWA Y., KACZICIESKI R.M., KING B.L.,

RAMAGIOTE D.R., MALLAIS L., MARCHIOLNI L., MCKENZIE L., MIKI H.,

RAMAGIOTE D.R., MALLAIS L., MARCHIOLNI L., MCKENZIE L., WIKI H.,

RAMAGIOTE D.R., MALLAIS L., MARCHIOLNI L., MCKENZIE L., WIKI H.,

RAMAGIOTE D.R., WALLAIS L., PORTIUS J.U., QI D., RAMACHADAR S.,

RAMAGIOTE D.R., WALLESCH R., PORTIUS J.U., QI D., RAMACHADAR S.,

RAYASSI T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RAMACHAR R., TAKENAR Y., TAYLOR M.S., TEARDAR R.,

RAMINING L.G., WYNSHAW-BORTIS A., YANG I., YANG I.,

RAMINING L.G., WYNSHAW-BORTIS A., YANGAYAMA T., FUKUGA S.,

SALIZANA T., WANDER T., KONDO H., NAKAMURA M., SAKAZUME N.,

SALIZANA T., WASHAR Y., KANANI J., ALAXAWA T., FUKUGA S.,

RAMINING L.G., WANDER Y., KANANI J., ALAXAWA T., FUKUGA S.,

RAMINING L.G., WANDER Y., KANANI J., ALAXAWA T., FUKUGA S.,

RAMINING L.G., WANDER Y., KANANI J., ALAXAWA T., FUKUGA S.,

RAMINING L., WANDER Y., KANANI J., ALAXAWA T., FUKUGA S.,

RAMINING L., WANDER W., IMPARANI J., ALAXAWA T., FUKUGA S.,

RAMINING L., WANDER W., ALAXAWA T., FUKUGA S.,

RAMINING L., WANDER W., IMPARANI Y., IMPARANI Y., RAYAWA I.,

RAMIAZAKI A., SAKAI K., KAWAI J., AINAWA T., FUKUGA S.,

RAMIAZAKI A., SAKAI K., KARANI J., AINAWA T., FUKUGA S.,

RAMIAZAKI A., SAKAI K., YANGANI J., AINAWA T., FUKUGA S.,

RAMIAZAKI A., SAKAI W., YANGANI W., SHIMBA S.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C5FBL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hisch F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-92064635; Pubmed-1955455;
Funayama N., Nagafuchi A., Sato N., Tsukita S., Tsukita S.;
"Radixin is a novel member of the band 4.1 family.";
J. Cell Biol. 115:1039-1048(1991).
                                         1; Indels
                                                                                                                                                 333 EREKEÇMMREKEBLMLRLÇDYEEKTRKAEKELSDÇIQRALK 373
                                                                                                        1 EREKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                               EZRI MOUSE STANDARD; PRT; 585 AA. P26040; Q802T8; Q9PC11; 01-MAY-1992 (Rel. 22, Created) 10-CCT-2003 (Rel. 42, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update)
       Pred. No. 1.7e-
                                                                                                                                                                                                                                                                                                                                                           585 AA
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VIL2.
                                         4,
   87.8%;
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                                         36; Conservative
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birney
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heltron E., Ketreman M., Madan A., Rodrigues S., Sanchez A., Hulting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz D., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.

-!- SUBCELULAR LOCATION: Cytoplasmic.

-!- TISSUE SPECIFICITY: Component of the microvilli of intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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82.9%; Pred. No. 4.8e-09;
iive 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY PDGFR) (BY SIMILARITY). PHOSPHORYLATION (BY PDGFR) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: Phosphorylated by tyrosine-protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structural protein, Cytoskeleton, Phosphorylation.
INIT MET 0 0 BY SIMILARITY.
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T -> A (IN REF. 1)
Q -> R (IN REF. 2)
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMEL; AKO02766; BAB22341.1; --
EMEL; BC048181; AAH48181.2; --
PIR; B41129; B41129; B41129; MGD; MGI: 98931; V412.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000799; EZ/rad/moesin.
Pfam; PF00773; Band 41; 1.
PRINTS; PR00955; BAND41.
SMART; SM00205; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Cytovillin) (Villin 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X60671; CAA43086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            585 AA;
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SEQUENCE
SOLUTION SOLUTION SERVICE SERV
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=92020840; PubMed=1924289;
Lankes W.T., Furthmayr H.;
"Mosein: a member of the protein 4.1-talin-ezrin family of proteins.";
Proc. Natl. Acad. Sci. U.S.A. 88:8297-8301(1991).
                                                                                                                 Goldenring J.R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane (By similarity).
-!-SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!-FTM: Phosphorylated by tyrosine-protein kinases (By similarity).
-!-SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 89.6%; Score 173; DB 1; Length 585; Best Local Similarity 82.9%; Pred. No. 4.8e-09; Matches 34; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-15; 53-59 AND 413-434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY PDGFR) (BY SIMILARITY). PHOSPHORYLATION (BY PDGFR)
   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
810FA26C69D7ED02 CRC64;
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01-MAG-1992 (Rel. 23, Last sequence update)
10-CCT-2033 (Rel. 42, Last amortation update)
Moesin (Membrane-organizing extension spike protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structural protein, CyToskeleton, Phosphorylation.
INIT MBT 0 0 BY SIMILARITY.
DOMAIN 1 294 FERM.
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Interpro; IPR000798; E2/rad/moesin.
Bam; PF00373; Band 41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF537266; AAN06818.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00935; BAND41.
PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
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                                                                                           SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                             NCBI_TaxID=9986;
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P26038;
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SEQUENCE FROM N.A.

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SECURINE-NOD; TISSUE=Thymus;

RA NEADLINE=2534683; PubMed=12466851;

RADINE=25354683; PubMed=12466851;

RADINE=25364683; PubMed=12466851;

RADINE=2536483; PubMed=12466851;

RADINE=25364683; PubMed=12466851;

RADINE=2536483; PubMed=12466851;

RADINE=2536483; PubMed=1246884851;

RADINE=25364834; R., Radino M., Richard M., Radino M., Radin
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVBAN, TISSUE=Breast tumor;

A treasberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rabolns=22388257; PubMed=12477937

A treasherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zebeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Brownstein M.J., Usdin T.B., Tonaldo M.F., Carvinci P., Prange C.,

Rab S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Mcraw P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Rale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Rale E.S., Low Y., Bouffard G.G.,

Rahey J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Rathey J., Helton B., Ketreman M., Madan A., Rodrigues S.,

Rather J., Helton B., Ketreman M., Schen E.D., Dickson M.C.,

Rather J., Schmutz J., Marza M.J.,

Rochiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rochiguez A.C., Grimwood J., Schmutz J., Marza M.A.,

Rochnerdia A. Schein J.E., Jones S.J.M., Marza M.A.,

Rochnerd A., Schein J.E., Jones S.J.M., Marza M.A.,

Rochnerd A. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                         "A gene family consisting of ezrin, radixin and moesin. Its specific localization at actin filament/plasma membrane association sites."; J. Cell Sci. 103:131-143(1992).
                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=93055012; PubMed=1429901;
Sato N., Funayama N., Nagafuchi A., Yonemura S., Tsukita S.,
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Moesin (Membrane-organizing extension spike protein).
                                                                                                                (Mouse)
                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                musculus
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Lankes W.T., Schwartz-Albiez R., Furthmayr H.,
Lankes W.T., Schwartz-Albiez R., Furthmayr H.,
"Cloning and sequencing of porcine moesin and radixin cDNA and
identification of highly conserved domains.",
Biochim. Biophys. Acta 1216:479-482(1993).
-!- FURCHION: Probably involved in connections of major cytoskeletal
structures to the plasma membrane.
-!- SIMILARITY: Contains 1 FERM domain.
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
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                                   66.8%; Score 129; DB 1; Length 57 illarity 63.4%; Pred. No. 4.8e-05; Conservative 9; Mismatches 6; Indels
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28-FEB-2003 (Rel. 41, Last annotation update)
Moesin (Membrane-organizing extension spike protein)
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FERM.
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InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Ez/räd/moesin.
InterPro; IPR008954; Moesin.
Pfam; PF00773; Band 41; 1.
Pfam; PF00769; ERM, 1.
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SMART; SM01295; B41; 1.
PROSITE; PS00060; PERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
Structural protein; Cytoskeleton.
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01-AUG-1992 (Rel. 23, Last seq
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es 26; Conservative
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                                Query Match
Best Local Similarity
Matches 26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scrofa (Pig)
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P26041;
                                                                                                                                                                                                                                                                                           RESULT 6
MOES PIG
ID MOES PIG
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RESULT 7
MOES MOUSE
ID MOES MC
AC P26041;
DT 01-MAY

Matches

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similarity).
-!- SIMILARITY: Contains 1 FERM domain.
 -!- PTM: Phosphorylated.
-!- SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                           InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Ez/räd/moesin.
Pfam; PF00373; Band 41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ249838; CAB59977.1; -.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Ez/rād/moesin.
InterPro; IPR008954; Moesin.
Pfam; PR00373; Band 41; 1.
Pfam; PR00769; ERM; 1.
                                                                                                                                                 EMBL; AF004811; AAB61666.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHICK
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                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDIJUE=20404065; PubMed=10945828;
Theobarides T.C., Wang L., Pang X., Letourneau R., Culm K.E., Basu S., Wang Y., Correia I.;
"Cloning and cellular localization of the rat mast cell 78-kDa protein phosphorylated in response to the mast cell 'stabilizer' cromolyn.";
J. Pharmacol. Exp. Ther. 294:810-821 (2000).
-!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
[4]
SEQUENCE OF 11-576 FROM N.A.
MEDINE=92243764; PubMed=1573844;
Furthmayr H., Lankes W.T., Amieva M.R.;
Furthmayr H., Lankes W.T., Amieva M.R.;
Mosein, a new cytoskeleral protein and constituent of filopodia: its
role in cellular functions.";
Kidney Int. 41:665-670(1992).
-!- FUNCTION: Probably involved in connections of major cytoskeletal
structures to the plasma membrane.
-!- SIMILARITY: Concains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Moesin (Membrane-Organizing extension spike protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EREKEGMMREKEELMLRLQDXEEKTKKAERBLSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EL -> DV (IN REF. 4).
RA -> SP (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structural protein; Cytoskeleton.
INIT MET 0 0 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                              MGD; MGI:97167; Msn.
InterPro; IPR000299; Band_4.1.
InterPro; IPR000798; E2/rad/moesin.
InterPro; IPR008954; Moesin.
Pfam; PF00373; Band_41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                            EMBL; S47577; AAA11762.1; -.
EMBL; AK088336; BAC40290.1; -.
EMBL; BC047366; AAH47366.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 371 R
576 AA; 67635 MW;
                                                                                                                                                                                                                                                                                                      EMBL; M86390; AAA39728.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INIT MET
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOES RAT
035763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE=20225478; PubMed=10760599;
Li W., Crouch D.H.; PubMed=10760599;
Li W., Crouch D.H.; Crouch D.H.; Crouch D.H.; Li W., Crouch B.H.; Li W., Crouch B.H.; Li W., Crouch B.H.; Li W., Crouch B.H.; Li B., Acta 1491:327-332(2000).
-!- FUNCTION: Probably plays a crucial role in the binding of the barbed end of actin filaments to the plasma membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 EKEKEKIEREKEELMEKLKOIEEQTKKAQQELEEQTRRALE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576 AA; 67607 MW; 59606907B2D89938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EREKEOMMREKEELMIRLODXEEKTKKAERELSEGIORALO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00935; BAND41.
PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
Structural protein; Cytoskeleton; Phosphorylation.
INIT_MET 0
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.3%; Score 126; DB 1; 61.0%; Pred. No. 9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
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68549 MW; 59AEA286DCAF7397 CRC64;

us-09-856-070b-29.std.rsp

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583 AA;
SQ SEQUENCE
                                 Query Match
                                                                    Matches
                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its word in institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERFORMANCE FROM N.A. Schwartz-Albiez R., Furthmayr H.;

Lankes W.T., Schwartz-Albiez R., Furthmayr H.;

Lichning and sequencing of porcine meesing of the biochim. Biophys. Action filaments to the plasma membrane.

Lichning and Schwartz-Albiez R. Concentral F. Checker R. Chec
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structural protein; CyToskeleton; Actin-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
     ·,
                                                                                                                                                                                        64.2%; Score 124; DB 1; Length 583; 61.0%; Pred. No. 0.00014; rive 9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                    1 EREKEGMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         583 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FERM.
GLU-RICH.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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InterPro; IPR000299; Band 4.1.
InterPro; IPR000789; Ez/Fad/moesin.
InterPro; IPR008954; Moesin.
Pfam; PF00373; Band 41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M86444; AAB02865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PSO0660; FERM 1; 1.
PROSITE, PSO0661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                              Local Similarity 61.0
nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Radixin (Moesin B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
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                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogene 8:1335-1345 (1935).

-!- FUNCTION: Probably plays a crucial role in the binding of the bankTION: Probably plays a crucial role in the binding of the barbed end of actin filaments to the plasma membrane.

-!- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE INTERPRENARE AND MITOTIC PRASE, RESPECTIVELY.

-!- PTM: Phosphorylated by tyrosine-protein Kinases.

-!- PTM: Contains I FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00935; BAND41.

PRABAT; SM00295; BAND41.

PROSITE; PS00660; FERM_1; 1.

PROSITE; PS00661; FERM_2; 1.

PROSITE; PS00661; FERM_3; 1.

Structural procesin; Cytoskeleton; Actin-binding; Phosphorylation; 3D-structure; Actin capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The ezrin-like family of tyrosine kinase substrates: receptor-specific pattern of tyrosine phosphorylation and relationship to malignant transformation.";
                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PHOSPHORYLATION.
STRAIN=BALB/c; TISSUE=Keratinocytes;
MEDLINE=93241736; PubMed=8479753;
Fazioli F., Wong W.T., Ullrich S.J., Sakaguchi K., Appella E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Liver;

MEDLINE-92064635; PubMed=1955455;

Funayama N., Nagafuchi A., Sato N., Tsukita S., Tsukita S.;

Funayama novel member of the band 4.1 family.";

J. Cell Biol. 115:1039-1048(1991).
      Length 583;
Match 62.7%; Score 121; DB 1; Length 56 Local Similarity 58.5%; Pred. No. 0.00026; les 24; Conservative 10; Mismatches 7; Indels
                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 28-53 AND 263-277
                                                                                                                                       1 EREKEÇMMREKEELMLRLQDXEEKTKKAERELSEÇIÇRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            583 AA
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PDB; IGC7; 28-JAN-03.

MGD; MGI:97887; Rdx.

InterPro; IPR000299; Band 4.1.

InterPro; IPR000799; E2/rad/moesin.

Pfam; PP00373; Band 41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X60672; CAA43087.1; -. PIR; A41129; A41129.
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                     __RADI MOUSE STANDARD P26043; Q9QW27; C1-MAY-1992 (Rel. 22, C 10-OCT-2003 (Rel. 42, L 10-OCT-2003 (Rel. 42, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Radixin (ESP10)
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TRHY RABIT P37709:
                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Nagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rachards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., I.,

Mhiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Human and minital analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilgenbus K.K., Milatovich A., Francke U., Furthmayr H.;
"Molecular cloning, cDNA sequence, and chromosomal assignment of the
human radixin gene and two dispersed pseudogenes.";
Genomics 16:199-206(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16893 (2002).

-!- FUNCTION: Probably plays a crucial role in the binding of the barbed end of actin filaments to the plasma membrane.

-!- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE CELL-TO-CELL ADDERENS UNCTTON AND THE CLEAVAGE FURROW IN THE INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.

-!- PTM: Phosphorylared by tyrosine-protein kinases (By similarity).

-!- SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                          .,
                                                                                                                            Length 583;
                                                                                                                                                         7; Indels
          GLU-RICH.
POLY-PRO.

EK -> VL (IN REF. 1).

E -> A (IN REF. 1).

R -> W (IN REF. 1).

R -> W (IN REF. 1).

R -> HA (IN REF. 1).
                                                                                                                                                                                                      334 EKEKERIEREKEELMERLRQIEEQTVKAQKELEEQTRKALE 374
                                                                                                                                                                                    1 EREKEOMMREKEELMLRLODXEEKTKKAERELSEGIORALO 41
                                                                                                                             62.2%; Score 120; DB 1; 58.5%; Pred. No. 0.00032;
                                                                                                                                                                                                                                                                                                 P35241; Q86v61;
01-FBS-1994 (Rel. 28, Created)
01-FBS-1994 (Rel. 28, Last sequence update)
Redixin.
                                                                                                                                                          10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
MEDLINE=93252378; PubMed=8486357;
                                                                                                    68600 MW;
                                                                                                                                                         24; Conservative
                                                                                                                                                                                                                                                                                     STANDARD;
 295
522
477
313
514
576
311
470
312
312
419
514
575
583 AA;
                                                                                                                                           Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                        HUMAN
                                                                     CONFLICT
                                          CONFLICT
                                                         CONFLICT
                                                                                                  SEQUENCE
                                                                                                                               Query Match
DOMAIN
DOMAIN
DOMAIN
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Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Intermediate filament-associated protein that associates in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair folliole and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodipeptide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even anchor the cell envelope to the KIF network. It may be involved in its own calcium-dependent postsynthetic processing during terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- TISSUE SPECIFICITY: Found in the hard keratinizing tissues such as the inner root sheath (IRS) of hair follicles and medulla, and in the filliform papillae of dorsal tongue epithelium (Probable).
-i- DEVELOPMENTAL STAGE: Expressed during late differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: Consists of nine domains. Domain 1 contains two EP-hand calcium-binding domains. Domains 2-4, 6, and 8 are almost entirely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00660; FERM_1; 1.
PROSITE; PS06661; FERM_2; 1.
PROSITE; PS06057; FERM_3; 1.
Structural protein; CyToskeleton; Actin-binding; Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.7%; Score 119; DB 1; Length 58
58.5%; Pred. No. 0.00039; Nicmatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K -> E (IN REF. 2).
889687EID675FFE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 EKEKERIEREKEELMERLKQIEEQTIKAQKELEEQTRKALE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EREKEQMMREKEELMLRLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1407 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLU-RICH.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:9944; RDX...
NIM; 179410; ...
Interpro; IPP000299; Band 4.1.
Interpro; IPR000798; Ez/rad/moesin.
Interpro; IPR00894; Moesin.
Pfam; PF00373; Band 41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Homodimer (Probable).
                                                                                                                                                                                                                                                                                           EMBL; L02320; AAA36541.1; -.
EMBL; BC047109; AAH47109.1; -.
                                                                                                                                                                                                                                                                                                                                                                           PIR; A46127; A46127.
Aarhus/Ghent-2DPAGE; 2501; IEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 328 K
583 AA; 68564 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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522
477
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the epidermis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actin capping.
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alpha-helical, configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 is the most regular and may bind KIF directly by ionic interactions. Domains 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                PTM: Substrate of transglutaminase. Some 200 arginines are probably converted to citrullines by peptidylarginine deimidase. SIMILARITY: In the N-terminal section; belongs to the S-100

        DOMAIN
        1
        91
        S-100 LIKE.

        2.2 BIND
        22
        33
        EF-HAND 1 (LOW AFFINITY) (POTENTIAL).

        CA BIND
        62
        73
        FF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

        SEQUENCE
        1407 AA, 183781 MW; AE17D2A159F12B7F CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.9%; Score 79; DB 1; Length 1407; 44.1%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P02633, 41CB.
InterPro; IPR001751; CaBP S100.
InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 1.
Pfam; PF00036; efhand; 1.
Prodom; PF00037; CaBP S100; 1.
PROSTTE; PS00307; CaBP S100; 1.
PROSTTE; PS00303; SIG CABP; 1.
Keratinization; Calcium-binding; Repeat; Citrullination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 REKEGMMREKEELMLRLQDXEEKTKKAERELSEG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-CCT-1994 (Rel. 30, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Trichohyalin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z19092; CAA79519.1; -. PIR; S28589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                              different species.
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15; Conserv
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SEQUENCE OF 1016-1549 FROM N.A.
STRAIN=Merino-Dorset horn X Border Leicester; TISSUE-Wool follicles;
MEDLINE=90130632; PubMed-258812;
Fietz M.J., Preeland R.B., Rogers G.E.,;
"The cDNA-deduced amino acid sequence for trichohyalin, a

SEQUENCE FROM N.A.
MEDLINE=33260018; PubMed=7684041;
Fietz M.J., McLaughlan C.J., Campbell M.T., Rogers G.E.;
"Analysis of the sheep trichohyalin gene: potential structural and calcium-binding roles of trichohyalin in the hair follicle.";
J. Cell Biol. 121:855-865(1993).

NCBI TaxID=9940;

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               Journal Biol. 110:427-436(1990).

J. Cell Biol. 110:427-436(1990).

J. Cell Biol. Intermediate filament-associated protein that associates in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair follicle and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodipeptide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even anchor the cell envelope to the KIF network. It may be involved in its own calcium-dependent postsynthetic processing during terminal
                                                                                                                                                                                                                                                                                                                                                                        Isolab22793-2; Sequence=VSP 000847, VSP 000848;
ISOSUE SPECIFICITY: Found in the hard keratinizing tissues such as the inner root sheath (IRS) of hair follicles and medulla, and in the pitchelia of the torgue, hoof and rumen.

DOMAIN: Consists of nine domains. Domain 1 contains two EF-hand calcium-binding domains. Domains 2.4, 6, and 8 are almost entirely alpha-helical, configured as series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 is the most regular and may bind KIF directly by ionic interactions. Domain 6 is commans 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among
differentiation marker in the hair follicle, contains a 23 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probably converted to cirullines by peptidylarginine deimidase. SIMILARITY: In the N-terminal section; belongs to the S-100
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EP-HAND 2 (HIGH AFFINITY) (POTENTIAL).
14 X 28 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       different species.
PTM: Substrate of transglutaminase. Some 200 arginines are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z18361; CAA70165.1; -.

R PIR; A40691; A40691.

R HSSP, P02633; 11G2.

R InterPro; IPR001751; CaBP_S100.

R InterPro; IPR002048; EF-hand.

R Ffam; PP01023; efhand.

R ProDom; PD003407; CaBP_S100; 1.

R PROSITE; PS00018; EF HAND; 1.

R PROSITE; PS00108; S100 CABP; RALSE NEG.

K Keratinization; Calcium-binding; Repeat; Citrullination;

M Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                        [soId=P22793-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-100 LIKE.
                                                                                                                                                                                                                                          SUBUNIT: Homodimer (Probable).
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CA_BIND
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Dermatol. 101:658-718(1993)
                                                                                                                                                                                                                                                        EMBL; L09190; AAA65582.1; -.
                                                                                                                                                         different species.
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73
390
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HSSP; P02633; 4ICB.
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1-11.
1-12.
1-13.
2 X Z3 AA APPRÒXIMATE TANDEM REPEATS.
2-1.
2-2.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          ď
                                                                                                                                                                                                                                                                                                                                                                                                        "The structure of human trichohyalin. Potential multiple roles as a functional BF-hand-like calcium-binding protein, a cornified cell envelope precursor, and an intermediate filament-associated (cross-
                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILIBE-93280194; PubMed=7685034;
Lee S.-C., Kim I.-G., Marekov L.N., O'Keefe E.J., Parry D.A.D.,
Steinert P.M.;
                                                                                                                                                                                                                                            .
9
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MEDLINE=93315897; PubMed=7686953;
O'Keefe B.U., Hamilton B.H., Lee S.-C., Steinert P.M.;
"Trichohyalin: a structural protein of hair, tongue, nail, and epidermis.";
                                                                                                                                                                                                                              38.9%; Score 75; DB 1; Length 1549; 40.5%; Pred. No. 9.8;
                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                1399 1399 E -> G (IN REF. 2).
1549 AA; 201173 MW; B72FB9FF1326E54E CRC64;
                                                                                                                                                                                  Missing (in isoform Short). /FTId=VSP 000847. Missing (in isoform Short). /FTId=VSP_000848.
                                                                                                                                                                                                                                                        3 EKEOMMREKEELMLRLQD-----XEEKTKKAERELSEQIOR 38
                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                     PRT; 1898 AA
                                                                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      envelope precursor, and an intermedi:
linking) protein.";
J. Biol. Chem. 268:12164-12176(1993)
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2-9.
2-10.
2-11.
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2-19.
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                                                                                                                                                                                                                                    Local Similarity 40.5
les 17; Conservative
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THH OR TRHY OR THL.
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Q07283;
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Matches
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FUNCTION: Intermediate filament associated protein that associates in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair follicle and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodipeptide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even anchor the cell envelope to the KIF network. It may be involved in its own calcium-dependent postsynthetic processing during terminal
                                                                                                                                                                                                                                                                                     the epidermis.

-i- DOWAIN: Consists of nine domains. Domain 1 contains two EF-hand calcium-binding domains. Domains 2-4, 6, and 8 are almost entirely alpha-helical, configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 is the most regular and may bind KIF directly by ionic interactions. Domains 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among
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EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
6 X 13 AA TANDEM REPEATS OF
R-R-E-G-E-E-E-R-R-E-Q-Q-L.
1 (APPROXIMATE).
1-2 (AAPPROXIMATE).
1-3 (AAPPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: Substrate of transglutaminase. Some 200 arginines are probably converted to citrullines by peptidylarginine deimidase.-!- SIMILARITY: In the N-terminal section; belongs to the S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA TANDEM REPEATS OF R-R-E-Q-Q-L
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MIN, 190370; CCYtoskeleton; NAS.

GO; GO: 0005509; F:calcium ion binding; TAS.

InterPro; IPR001751; CaBP_S100.

R InterPro; IPR002048; EF-hand.

InterPro; IPR002048; EF-hand.

R Ffam; PF00036; Efhand; 1.

R PROSITE; PS00036; EFABND: 1.

R PROSITE; PS00039; SI00; 1.

R ROSITE; PS000018; EF HAND: 1.

R ROSITE; PS000018; EF HAND: 1.

R KERTINIZATION; Calcium-binding; Repeat; Citrullination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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1-5.
2-2.
2-2.
2-4.
2-5.
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                               444 702 9 X 28 AA APPROXIMATE TANDEM REPEATS.
923 1162 4-1
923 952 4-1
953 982 4-2
1013 102 4-3
103 1102 4-5
1103 1132 4-7
1133 1162 4-6
1155 1849 23 X 26 AA APPROXIMATE TANDEM REPEATS.
1752 1752 1752 F -> L (IN REF. 2).
1754 1801 QERDRQYR -> RSETGSTG (IN REF. 2).
1857 1857 QERDRQYR -> RSETGSTG (IN REF. 2).
1868 1867 1857 Q -> K (IN REF. 2).
1869 AA; 247219 MW; A74B5947FB62E31D CRC64;
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                    2-9.
9 X 28 AA APPROXIMATE TANDEM REPEATS.
8 X 30 AA TANDEM REPEATS.
4-1.
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Search completed: August 16, 2004, 09:44:10 Job time : 13 secs

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August 16, 2004, 09:43:56 ; Search time 77 Seconds (without alignments) 168.003 Million cell updates/sec
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1 EREXEQMMREXEELMLRLQD......BEKTKKAERELSEQIQRALQ 41
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1: Sp archea:*
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
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Maximum DB seq length: 2000000000
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Sequence:
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	!	QI	Q8CBU4	Q8VHK3	O9YGW6	Q7ZWC7	Q9PT71	920160	Q9UJZ7	Q9UJZ8	Q9UK20	Q7TSG6	Q9UJZ2	088735	Q7TQL9	Q8N7Z2	Q8N9W4	V GT /100
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оNo	Query	Match	89.6	89.6	83.9	9.09	57.0	53.9	52.8	47.7	47.7	46.1	45.1	38.9	38.9	38.6	38.1	0 6
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Gaps

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Query Match 89.6%; Score 173; DB 11; Length 421; Best Local Similarity 82.9%; Pred. No. 4.3e-10; Matches 34; Conservative 6; Mismatches 1; Indels C

Q8cf87 mus musculu Q8n824 homo sapien Q25777 plasmodium Q265777 plasmodium Q265777 plasmodium Q26003 drosophila Q29u0d5 tetrahymena Q29vyu0 drosophila Q26dx6 plasmodium Q8dx6 plasmodium Q8dx6 plasmodium Q8nv21 homo sapien Q2nv212 homo sapien Q7z22 homo sapien Q7x22 homo sapien Q56D1 oryza sativ Q96D1 babesia big Q8132 caenorhabdi Q7xwf1 plasmodium Q8145 homo sapien Q8140 homo sapien Q8140 mus musculu Q80tu6 mus musculu Q8140 homo sapien Q8140 homo sapien Q8140 homo sapien Q8140 homo sapien		date) update)	rata; Euteleostomi; ridae; Murinae; Mus.	ase I & II Team; functional annotation of 7 CRC64;
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		PRELIMINARY (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. agment)	ô	1188 1188
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733 733 711.5 711.5 711.5 711.5 711.5 711.7 71.5 70 70 70 70 70 70 70 70 70 70 70 70 70		LT 1  14  08 CBU4  08 CBU4;  01 -MAR-2003  01 -MAR-2003  01 -OCT-2003  Villin 2 (F.	Mus musculus (Mous Bukaryota; Metazoa Mammalia; Butheria NCBI_TaxID=10090;	SECUENCE FROM N.A. STRAIR=CSTBL/6J; TISSUE=Urinar, MEDLINE=22354683; PubMed=12466 The FANTOM CONSORTIUM, the RIKEN Genome Exploration Re 60,770 full-length cDNAs."; Malysis of the mouse transcr. 60,770 full-length cDNAs."; EMBL; AKO35271; BAC20093.; MGD; MGI:98931; Vil2. InterPro; IPR00059; Band 4.1. InterPro; IPR00854; Mossin. PFam; PF00769; BRM; 1, 1. PROSITE; PS00661; FERM 2; 1. PROSITE; PS00661; FERM 2; 1. PROSITE; PS00657; FERM 2; 1. NON TER. SEQUENCE 421 AA; S0273 WW;
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"Specific expression of ezrin, a cytoskeletal-membrane linker protein,
"Specific expression of ezrin, a cytoskeletal-membrane linker protein,
in a subset of chick retinotectal and sensory projections.";
Eur. J. Neurosci. 11:545-556(1999).
EMBL; AB019790; BAA7497.11. .

GO; GO:0005856; C:cytoskeleton; IEA.
InterPro; IPR000299; Band 4.1.
InterPro; IPR0009954; Moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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89.6%; Score 173; DB 11; Length 455;

Best Local Similarity 82.9%; Pred. No. 4.6e-10;

Matches 34; Conservative 6; Mismatches 1; Indels
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A Gunn-Moore F.J. Tait S., Brophy P.J.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF450298; AAL47844.1; -
C GO, GO, GOOGS866; C:Cytoskeleten; IEA.
InterPro; IPRO00799; Band 4.1.
InterPro; IPRO00799; EZ/rad/moesin.
PERM; PRO00373; Band 4.1.
PRINTS; PRO0935; BAND41.
SPRAT; SMO0295; BAN, 1.
PROSITE; PSO0661; FERM, 1; 1.
PROSITE; PSO0661; FERM, 1; 1.
PROSITE; PSO0661; FERM, 2; 1.
PROSITE; PSO0661; FERM, 3; 1.
NOW TER
PROSITE: PSO0661; FERM, 3; 1.
PROSITE; PSO0661; FERM, 3; 1.
PROSITE; PSO0661; FERM, 3; 1.
                                                        169 EREKEÇMLREKEELMLRLQDYEQKTKRAEKELSEQIEKALQ 209
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                         455 AA
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MEDLINE=99171943; PubMed=10051754;
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Pfam; PF00769; ERM; 1.
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                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ezrin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                        Q8VHK3;
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                                                                                                                                                                                                                                                                                                                                         Q8VHK3
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Q9YGW6
                                                                                                                                                                                                                                  RESULT 2
Q8VHK3
                                                                                                                                                                                                                                                                                                                                                                                             SQ DER REPORTED TO THE PROPERTY OF THE PROPERT
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01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Brachydanio rerio (Zebrafish) (Danio rerio).
Brakryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Actinopterygii; Neopterygii; Teleostei, Ostariophysi; Cypriniformes, Cyprinidae, Danio.
NCBL_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                                                                                                                                Length 585;
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO49479; AA449479; 1...
R GO; GO:0005856; C:cytcoskeleton; IEA.
InterPro; IPR000299; Band 4.1.
R InterPro; IPR000299; Band 4.1.
R Pfam; PF00373; Band 4.1; 1.
P Pfam; PF00373; BAN41.
R Pfam; PF00769; ERM; 1.
R PRANT; SM00295; B41; 1.
R PROSITE; PS00660; FERM 1; 1.
R PROSITE; PS00661; FERM 2; 1.
                                                                                                                                                                                                                                                                      Indels
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PRINTS, PR00935; BAND41.

SMART; SM00295; B41; 1.

PROSITE; PS00660; FERM 1; 1.

PROSITE; PS50061; FERM 2; 1.

PROSITE; PS50077; FERM 3; 1.

SEQUENCE 585 AA; 69366 MW; 854C6348F783CAEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 439 439 MW; 8C907EB06D0A3D12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         334 EREKEÇMLREKEELLVRLQEYEVKTKRAEKELSDQIQRALQ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 EKEKEKIEKEKEELMERLRVIEEQTRKAQQELEEQTRKALE 374
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                                                                                                                                                                                                                                                                                                                                   1 EREKEOMMREKEELMLRLQDXEEKTKKAERELSEQIORALQ 41
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                                                                                                                                                                                                            83.9%; Score 162; DB 13;
78.0%; Pred. No. 7.7e-09;
tive 7; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
60.6%; Score 117; DB 13;
Best Local Similarity 56.1%; Pred. No. 0.00024;
Matches 23; Conservative 12; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 AA
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                Query Match
Best Local Similarity 78.09
Matches 32; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE
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156 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EREKEOMMREKEELMLRLQDXE 22
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nes 19; Conservative
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SEQUENCE FROM N.A.
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Matches
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

NOBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Fadiel A., Chen Z.C., Naftolin F.;
Fadiel A., Chen Z.C., Naftolin F.;
Mutation of ezrin gene in cancer.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF189213; AAF03156.1; -.
GO, GO:0005856; C:Cytoskeleton; IEA.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; EZ/rad/moesin.
Pfam; PF00769; ERM; 1.
PROSITE; PS50057; FERM_3; 1.
Armstrong N.A., Thorn J.M., Kay B.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
BMBL; U29763; AAF21215.1.
GO; GO:0005855; C:cytoskeleton; IEA.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Ez/rad/moesin.
InterPro; IPR008954; Moesin.
Pfam; PF00779; Band 41; 1.
                                                                                                                                                                                                                                                             PRINTS; PR00935; BAND41.
SWART; SW00295; B41; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
SEQUENCE 580 AA; 68134 MW; 1006A7E9E5887074 CRC64;
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159 AA; 19234 MW; 7C398388B7BA70FA CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNJ-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment)
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Q9UJZ6;
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Q9UJZ7
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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A Chen Z.C., Fadiel A., Naftolin F.;
Chen Z.C., Fadiel A., Naftolin F.;
"Mutation of ezrin gene in cancer.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
R GO, GO:000596; GY:00596; GY:00596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 52.8%; Score 102; DB 4; Length 158; Local Similarity 95.5%; Pred. No. 0.0033; les 21; Conservative 0; Mismatches 1; Indels
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TISSUE-ovary;
Chen Z.C., Fadiel A., Naftolin F.;
Ezrin gene mutation in ovarian cancer.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF188897; AAF03155.1; -..
GO; GO:0005865; C:cytoskeleton; IEA.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Ez/rad/moesin.
PROSITE; PSS0057; FERM; 1.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment).
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7; Mismatches
                                             1 EREKEOMMREKEELMIRLODXBEKTKKAER 30
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MTAP7 OR MAP.
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last anno
                                                                                                                                                                                                                                                             Created)
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 100.
Matches 18; Conservative
18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jonca J.,
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Q9UJZ2
  Matches
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TISSUE-Testicle;

RADINE-238825;

PUDDINE-238825;

REDINELNE-238825;

RADINE-238825;

RADISTOR R.P., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Rischul S.P., Zeeberg B.M., Buetow K.H., Schaefer C.F., Baata N.K., Androhenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Staplecon M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E., Staplecon M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Rada S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Hulting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anthering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anthering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anthering M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Radriquez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human
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                                                TISSUE-Placenta;
A Chen Z.C., Fadiel A., Naftolin F.;
Mutation analysis of ezrin gene in cancer cells.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RMBL; AF187552; AAD56713.1; -.
RMBL; AF187552; AAD56713.1; -.
GO, GO:0005856; C:C:ytoskeleton; IEA.
InterPro; IPR000799; Ez/rad/moesin.
R Pfam; PP00137; Band 4.1.
R Pfam; PP00137; BRM, 1.
R Pfam; PP00775; FRM, 1.
R Pfam; PP00776; FRM, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 92; DB 4; Length 161;
Pred. No. 0.035;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Testicle;
Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC053417; AAH53417.1; -.
Hypochetical protein.
BROUSNCE 389 AA; 46367 MW; 6EA2EDCBA9BB5A76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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100.0%; Pred. No. v..
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity
       [1]
SEQUENCE FROM N.A.
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01-OCT-2003 (
01-OCT-2003 (
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"The distribution of murine 115-kDa epithelial microtubule-associated protein (R-MAP-115) during embryogenesis and in adult organs suggests a role in epithelial polarization and differentiation.";
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
Chen Z.C., Fadiel A., Naftolin F.;
Mutation of cytovillin gene in glioblastoma.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF190059; AAF03158.1;
EMBL; AF190059; AAF03158.1;
InterPro; IPR000799; Band 4.1.
InterPro; IPR000798; Ez/rad/moesin.
PRONTE; PSD0057; FERM, 1.
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  Indels
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152 AA; 18416 MW; B7FCE817DD2B9291 CRC64;
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Last annotation update)
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Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ40199.
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tes 18; Conservative
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Best Local Similarity 42.5
Matches 17; Conservative
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                                                                                                                                           (Human)
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                                                                                                                                        Homo sapiens
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Q8N9W4;
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Q8N9W4
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  HERE REAL SERVICE SERV
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                           2;
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                                                                                                                                                                                                                    Score 75; DB 11; Length 730; Pred. No. 7.7;
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                                                                                                                                                                                                                                                                        9; Indels
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(DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                     Interpro; IPR008604; E-MAP-115.
Pfam; PF05672; E-MAP-115; 1.
SEQUENCE 730 AA; 82021 MW; F44B4201DE8F5A17 CRC64;
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SEQUENCE 738 AA; 82839 MW; BFA2DIEICC78815F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to microtubule-associated protein 7.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                            2 REKEOMMREKEELMLRLQDXEEKTKKAERELSEQIOR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 REKEGMMREKEELMLRLQDXEEKTKKAERELSEGIQR 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         738 AA.
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                                                                                                                                                                                                                                                                        8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                       EMBL; Y15197; CAA75495.1; -. EMBL; AB098611; BAC53729.1; -. MGD; MGI:1328328; Mtap7.
                                                                                                                                                                                                                    38.9%;
                                                                                                                                                                                    Query Match
Best Local Similarity 48...
Best Local 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 48.6
es 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Eye;
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7TQL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8N7Z2
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
Q7TQL9
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Q8N7Z2
ID Q8N7Z
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Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., Ishidashi T., Kanehori K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                             Kawakani B., Sugiyama A., Takemoto M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Sato H., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma P., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshina A., Suzuki Y., Supan S., Nagahari K., Masuho Y., Magai K., Isogai T.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, AKO97517, BACC0504-17.

BILINEPPO, IPRO00533, Tropomyosin.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 REKEQMMREKEELML------RLQDXEEKTKKAERELSEQIQRALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.6%; Score 74.5; DB 4; Length 621; 35.3%; Pred. No. 7.5; tive 11; Mismatches 11; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK093463; BAC04173.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
Hypothetical protein.
Hypothetics 650 AA; 79069 MW; 2DCE6078E002D031 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                621 AA; 77106 MW; 67938434F3BE7929 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 REREKKMREEEETM----REQEEKMOKQEENWWEQEEKEWQ 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 REKEOMMREKEELMIRLODXEEKTKKAERELSEQIORALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.1%; Score 73.5; DB 4;
42.5%; Pred. No. 9.9;
tive 9; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein FLJ36144.
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Search completed: August 16, 2004, 09:45:40 Job time: 78 secs

us-09-856-070b-29.std.rspt

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August 16, 2004, 09:50:52; Search time 55 Seconds (without alignments) 210.626 Million cell updates/sec
                                                                                                                                                                                                                                 1 BREKEQMMREKEELMLRLQD......EEKTKKAERELSEQIQRALQ
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                   1586107 segs, 282547505 residues
                                                                             using sw model
                                                                                                                                                                                                                                                                        OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                           US-09-856-070B-29
                                                                           - protein search,
                                                                                                                                                                                           Title:
Perfect score:
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Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Word size :

geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Human nov Human col Human hep Novel hum Human hep Human hep Human Bre Human hep Amino aci Human hep Photorhab Human Pro Amino aci Human nov Novel hum Human Human Novel Description Aab82020 I Aag73954 I Adc31630 I Adu30004 Add31631 Add31631 Add31631 Add33060 Add33060 Add30038 Add2038 Add2038 Add22984 Add22984 Add22984 Add0224 Add0 Aay27443 Adc31629 Ade63987 ADC31631 AAB53356 AAB82035 AAU33060 AAB82037 AAB82038 AAU68025 AAB82039 AAB07823 Length DB 510 510 510 510 555 555 Query Match Result 8

The present sequence is domain B of human hepreceptor of human ezrin. The presceptor is a novel active site in human ezrin. Bzrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see AABB2021 to AABB2041) that bind to hepreceptor with greater affinity than HEP1 (see immune response, and for treating peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present sequence assembles into two anti-parallel

Streptoco Human Pro Human NOV Human NOV

Abg61631 Ade54611

ABO15000 ABO15001 ABG61631 ADE54611

Claim 5; Page 36; 42pp; English.

5108	27	Adb70362 Moesin SE	Adc77532 Human moe	Abu89709 Protein d	Adb79911 Mouse put	Murine	Novel		Aaw71293 Protein G	Adb65482 Human pro	Aay53008 Human sec	Aae01020 Human pif	Aab24238 Human ves	Aab93007 Human pro	Aab95640 Human pro	Aae22856 Human his	Aau99661 Human His	Adc21697 Human his	Add14124 Human src
ADD45108	ABR59727	ADB70362	ADC77532	ABU89709	ADB79911	ADC56738	ABG19947	AAW22780	AAW71293	ADB65482	AAY53008	AAE01020	AAB24238	AAB93007	AAB95640	AAE22856	AAU99661	ADC21697	ADD14124
7	9	7	7	9	7	7	4	N	(7)	7	ო	4	m	4	4	Ŋ	2	7	7
576	577	577	577	583	583	583	593	645	645	650	667	689	742	796	817	1215	1215	1215	1272
17.1	17.1	-	7	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1	17.1
7	۲	7	7	7	^	1	7	7	7	7	7	7	7	7	7	7	7	7	7
26	27	28	2 6	30	31	32	33	34	35	36		38	39	40	41	42	43	44	45

## ALIGNMENTS

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Human; hepreceptor domain B; cytostatic; anti-HIV; antibiotic; nootropic;
immune response inducer; ezrin; infectious diseases; cancer;
HIV-related dementia.
                                                                                                                                                                                                                                                                             Novel regulatory or unfolding peptides of ezrin that binds to Hepreceptor, useful for inducing immune response for treating infectious diseases and cancer.
                                                                                                                                        /note= "Optionally phosphorylated"
                                                                                                                      Location/Qualifiers
AAB82020 standard; peptide; 34 AA.
                                                                                                                                                                                           99GB-00021881
                                                                                                                                                                                                           99GB-00021881
                                                  Human hepreceptor domain B.
                                  (first entry)
                                                                                                                                                                                                                                                              WPI; 2001-293287/31
                                                                                                                                                                                                                             Ж
О
                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                             (HOLM/) HOLMS
                                                                                                                                                                                           17-SEP-1999;
                                                                                                       Home sapiens
                                                                                                                                                                                                           17-SEP-1999;
                                  13-JUN-2001
                                                                                                                                                        3B2354241-A
                                                                                                                                                                           21-MAR-2001
                                                                                                                                                                                                                                              Holms RD;
                 AAB82020;
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Human novel polypeptide sequence, SEQ ID NO:1712.

(first entry)

18-DEC-2003

ADC31630;

ADC31630 standard; protein; 579 AA

RESULT 3

184 EREKEÇMMREKEELMLRLÇD 203

B

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cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic acityity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used in the prevention, diagnosis cample, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that ffect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally. N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host colon cancer-associated Ps, by inserting the nucleic acids into a host call and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AMH37196 to AMH37204 and AMB7789 represent sequences used in the exemplification of the present invention. N.B pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                  Length 34;
                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein SEQ ID NO:4718.
                                                                              Ouery Match

48.8%; Score 20; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 20; Conservative 0; Mismatches 0;
helices with hepreceptor domain A (see AAB82019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 6520-6521; 9803pp; English.
                                                                                                                                                                                                                                                                                                             AAG73954 standard; protein; 436 AA
                                                                                                                                                                  22 EEKTKKAERELSEQIORALO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birse CE,
                                                                                                                                                                                                       15 EEKTKKAERELSEQIORALO 34
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99US-0163280P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                co 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-235357/24.
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                                           Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200122920-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                       AAG73954;
                                                                                                                                                                                                                                                                      RESULT 2
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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC3089-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or ameliorating a medical condition, kits comprising polynuclectide probes and/or monoclonal antibodies for carrying out the methods of the invention, methods for the identification of compounds that modulate the invention; methods for the identification of compounds that modulate the invention; methods for the polynuclectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628 contig sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, drug screening, forenation, gene mapping, in the identification of mutations responsible for genetic disorders or other treating blodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                             Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; nameurodegenerature diseases; anameia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; meturoprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatiic; gene therapy; chromosome 6q25.2-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ren F, Xue AJ, Zhao QA, Wang J,
Wang D, Ma Y, Asundi V, Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 1712; 1185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-2001; 2001US-0324631P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                        disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The mucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmet directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
disease and other neurodegenerative diseases, anaemia, platelet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 48.8%; Score 20; DB 7; Length 579; Local Similarity 100.0%; Pred. No. 2.2e-11; les 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Befort K, Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Protein P15311, SEQ ID NO 9933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE63987 standard; protein; 585 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 BREKEOMMREKBELMLRLOD 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EREKEOMMREKEELMLRLOD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-268312/26.
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 579 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003016475-A2.
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ADE 53987

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         polymucleorides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polypeptides given in the open polypeptides or their antibodies. The polypeptide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at fip, wipo. int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /notes "the Tyr at this position can be mutated (preferably to a Phe) to construct an ezrin mutant of the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a pharmaceutical composition containing ezrin protein, RNA or DNA mutated on tyrosine 353, or a functional fragment or derivative of the ezrin mutant. The new composition is useful for prevention and/or treatment of tumors, and especially metastasis. The present sequence represents the amino acid sequence of human ezrin (before the maturation by deletion of the first amino acid Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition for prevention and treatment of tumors and metastasis.
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compound that regulates the activity of one or more of the
                                                                                                                                                                                                                                                                                                                               Length 585;
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                                                                                                                                                                                                                                                                                                                             48.8%; Score 20; DB 7; Le
100.0%; Pred. No. 2.3e-11;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of human ezrin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louvard D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gautreau A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY27443 standard; protein; 586 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           333 EREKEÇMMREKEBLMLRLÓD 352
                                                                                                                                                                                                                                                                                                                                           100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                      1 EREKEOMMREKEELMLRLOD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 1; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURI-) INST CURIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-EP002054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                              Sequence 585 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY27443;
                                                                                                                                                                                                                                                                                                                                 Query Match
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Sequence 586 AA;

cuseful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other trained. Training blodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disorders, wounds, burns, ulcers, osteoporcois, ancemia, platelate disorders, wounds, burns, ulcers, osteoporcois, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence of data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the print of the print

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Gaps

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Gaps .

DB 7; Length 611; 2.3e-11; 0; Indels

100.0%; Pred. ... 48.8%; Score 20; 100.0%; Pred. No.

to...
Best Local Similarity 100.0
Matches 20; Conservative

Sequence 611 AA;

1 EREKEOMMREKEELMLRLQD 20

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New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                        Human, diagnostic, drug screening; forensics, gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; antenime disease; cancer; molecular weight marker; food supplement; antiparkinsonian; mootropic; melecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprofective; antianaemic; anti-coagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 625.2-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wehrman T;
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Wang Z, Weng G;
48.8%; Score 20; DB 2; Length 586; 100.0%; Pred. No. 2.3e-11; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  Human novel polypeptide sequence, SEQ ID NO:1711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang J, Ren F, Xue AJ, Zhao QA,
Shosh M, Wang D, Ma Y, Asundi V,
ente D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 1711; 1185pp; English.
                                                                                                                                                ADC31629 standard; protein; 611 AA
                                                                             334 EREKEÇMMREKEELMLRLÇD 353
                                                      20
                                                      1 EREKEQMMREKEELMLRLQD
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                                                                                                                                                                                                     (first entry)
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-371981/35.
               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ghosh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haley-Vicente D,
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                                                                                                                                                                                                                                                                                                                                                                                                         WO2003029271-A2.
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                           20;
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Zhou P, G
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 Query Match
                           Matches
                                                                                                                       RESULT 6
                                                                                                                                      ADC31629
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The invention relates to novel human secreted polypeptides. The polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                             Human, vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 219; 765pp; English.
                                                                                        AAU30004 standard; protein; 622 AA
                                                                                                                                                                                             Novel human secreted protein #495.
334 EREKEOMMREKEELMIRLOD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT;
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26-JAN-2001; 2001US-00770160.
                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                             18-DEC-2001
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                                                                                                                         AAU30004;
                                                                                                                                                                                                                                 Human;
                                                                     AAU30004
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The invention relates to 971 novel human cDNA sequences (ADC29919-CD20889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of polynucleotides or polypeptides of the invention; and methods of invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the invention of compounds that modulate the invention; methods for the invention of compounds that modulate the invention; methods for the dentification of compounds that modulate the expression or activity of the polynuclectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC33628) -ADC33394). The nucleic acids and polypeptides of the invention are

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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody polynucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon sind/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29910-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; uneurodegenerative disease; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease, cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; antenceptective; antieneemic; anticoagulant; thrombolytic; vulnerary; antiulocupressive; antiinflammatory; cytostatic; gene therapy; chromosome 6q25.2-26.
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                                                                                                                                                                             Length 622;
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Pred. No. 2.4e-11;
0; Mismatches 0; Indels
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Wang Z, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human novel polypeptide sequence, SEQ ID NO:1713.
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Asundi V,
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Wang D, Ma Y, A
                                                                                                                                                                                                                                                                                                                                                                            ADC31631 standard; protein; 628 AA
                                                                                                                                                                  48.8%; SCC_
100.0%; Pre
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                                                                                                                                                                                                                                                  1 EREKEOMMREKEELMLRLOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                 Conservative
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N-PSDB; ADC30660.
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                                                                                                                                                                                            Local Similarity
nes 20; Conserv
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Zhou P, Ghosh M,
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                                                                                                                                               Sequence 622 AA;
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                                                                                                                                                                                   Query Match
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invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polynuclectide probes and/or monoclonal antibodies for carrying out the methods of the cinvention; methods for the identification of compounds that modulate the expression or activity of the polynuclectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention of (ADC31361-ADC3262) and the polypeptides encoded by the contigs (ADC31361-ADC3324). The nucleic acids and polypeptides of the invention are cuseful in diagnostics, drug screening, forensics, gene mapping, in the contists, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's cisacase and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoliment assessing corrients. The public periodic primers and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically and shown in electronic format directly from WIPO at the invention, but were contained in a fortuning matt of the printed specification, but the contained and are decombined discases. The sequence of the invention. Note: The sequence of the invention of the printed specification, but the contained and are decombined and are decombined by the contained and are decombined and are decombined by the contained and are decombined and are decombined and are decombined and are decombined by the contained and are decombined and are decombined by the contained and are decombined and and are decombined by the contained and are decombined by the contained and are decombined by the contained and are decombined by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; general disorder; renal disorder; infectious disease; cardiovascular disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein sequence SEQ ID NO:896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Pred. No. 2.4e-11;
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Best Local Similarity
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hepreceptor (AAB82019 and AAB82020)

Sequence 14 AA;

SXS

called human colon cancer antigens, given in AAB52234 to AAB5406. The human colon cancer antigens can have cytostatic, cardioactive, muscular, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, infectious diseases, and cardiovascular disorders, infectious diseases; and cardiovascular disorders and AAB54007 represent sequences used in the exemplification of the present invention AAC97991 to AAC98763 encode the human colon cancer associated proteins, Claim 11; Page 1449-1451; 2104pp; English. 

Sequence 635 AA;

Gaps .. 0 48.8%; Score 20; DB 3; Length 635; 100.0%; Pred. No. 2.4e-11; ive 0; Mismatches 0; Indels 20; Conservative Local Similarity Query Match Best Loca Matches

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AAB82035 standard; peptide; 14 AA. RESULT 10 AAB8203 

AAB82035;

(first entry) 13-JUN-2001

Human hepreceptor domain A/B binding peptide Rupe1024.

Human; hepreceptor; cytostatic; anti-HIV; antibiotic; nootropic; immune response inducer; ezrin; infectious diseases; cancer; HIV-related dementia.

Homo sapiens

GB2354241-A

21-MAR-2001

99GB-00021881 17-SEP-1999; 99GB-00021881 17-SEP-1999;

(HOLM/) HOLMS

Holms RD;

WPI; 2001-293287/31

Novel regulatory or unfolding peptides of ezrin that binds to Hepreceptor, useful for inducing immune response for treating infectious diseases and cancer. The hepreceptor is a novel active site in human ezrin. Ezrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see ABB2021 to AAB82041) that bind to hepreceptor with greater affinity than HEPI (see AAB82046). The hepreceptor binding peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present peptide binds to domains A and B of the Claim 20; Page 36; 42pp; English.

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Gaps

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29.3%; Score 12; DB 4; Length 52; 100.0%; Pred. No. 0.00019; ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.0
Matches 12; Conservative

Sequence 52 AA;

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AUC29510-AAU33304 represent the amino acid sequences of novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                Human, vaccination; gene therapy, nutritional supplement,
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                     Gaps
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 Length 14;
34.1%; Score 14; DB 4; Length 14;
100.0%; Pred. No. 6.6e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                 Novel human secreted protein #3551.
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                                                                                                                                                                                           AAU33060 standard; protein; 52 AA.
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26-JAN-2001; 2001US-00770160
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les 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
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The hepreceptor is a novel active site in human ezrin. Ezrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see AAB82021 to AAB82041) that bind to hepreceptor with greater affinity than HEP1 (see AAB82046). The hepreceptor binding peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present peptide binds to domain A of the hepreceptor (AAB82019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Breast cancer-associated protein isoform, BPI-1 peptide #3
                             Human, hepreceptor; cytostatic, anti-HIV; antibiotic; nootropic; immune response inducer; ezrin; infectious diseases; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Breast cancer-associated protein isoform; breast cancer; immunogen; cytostatic; BPI; tryptic digest peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel regulatory or unfolding peptides of ezrin that binds to Hepreceptor, useful for inducing immune response for treating diseases and cancer.
Human hepreceptor domain A binding peptide Rupe2132.
                                                                                                                                                                 /note= "Optionally phosphorylated"
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100.0%; Pred. No. 0.0
:ive 0; Mismatches
                                                                                                                                 Location/Qualifiers
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9; Conservative
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                                                                  HIV-related dementia.
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                                                                                                                                                 Modified-site
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                                                                                                     Homo sapiens
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel regulatory or unfolding peptides of ezrin that binds to Hepreceptor, useful for inducing immune response for treating infectious diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The hepreceptor is a novel active site in human ezrin. Ezrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see AAB82021 to AAB82041) that bind to hepreceptor with greater affinity than HEP1 (see AAB82046). The hepreceptor binding peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present peptide binds to domain A of the hepreceptor (AAB82019)
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                                                                                                                                                                                                                                                   Human; hepreceptor; cytostatic; anti-HIV; antibiotic; nootropic; immune response inducer; ezrin; infectious diseases; cancer; HIV-related dementia.
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                                                                                                                                                                                                                      Human hepreceptor domain A binding peptide Rupe2032
                                                                                                                                                                                                                                                                                                                                                                                         "Optionally phosphorylated"
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                                                                                                                         AAB82037 standard; peptide; 13
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Modified-site
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AAB82037
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DB 4; Ler., No. 0.046; 0; Indels

infectious

(OXFO-) OXFORD GLYCOSCIENCES UK LTD

20-MAR-2000; 2000GB-00006695. 24-MAR-2000; 2000GB-00007265.

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The invention relates to diagnosing, determining the stage or severity, or identifying the risk of a subject developing cancer (especially breast cancer), or monitoring the effect of therapy on a subject with cancer, comprising analysing a test sample using two-dimensional electrophoresis and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The methods disclosed are used for the diagnosis and prognosis of breast cancer, and concer, it cancer, for determining the severity of breast cancer, and monitoring the effect of therapy administered to a subject Antibodies raised against the binding domain of a BPI, and the composition for treating or preventing breast cancer. The methods use sensitive and specific biomarkers provide early diagnosis of breast cancer, and the fewer side effects that other prior art methods. The present sequence is a tryptic digest peptide from a BPI of the invention
                                                                                                                                                                                                                                                                                                                 Identifying proteins for clinical screening, diagnosis and prognosis
breast cancer, comprises detecting Breast Cancer-Associated Protein
Isoforms (BPIs) using two-dimensional electrophoresis.
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                                                                                                                                                                         Waterfield MD
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                                                                                                                                                                         Parekh RB,
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                                                                                                                                                                             Page MJ,
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Matches 8; Conservative
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Novel regulatory or unfolding peptides of ezrin that binds to
Hepreceptor, useful for inducing immune response for treating infectious
                                                                                                                                                                                                         The hepreceptor is a novel active site in human ezrin. Ezrin regulates the structure of the cortical cytoskeleton to control cell surface topography. The present invention relates to peptides (see AAB82021 to AAB82041) that bind to hepreceptor with greater affinity than HEP1 (see AAB82046). The hepreceptor binding peptides are useful for inducing immune response, and for treating infectious diseases, cancer and HIV-related dementia. The present peptide binds to domain A of the hepreceptor (AAB82019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: August 16, 2004, 09:54:33 Job time : 56 secs
                                                                                                                                                                        Claim 26; Page 37; 42pp; English
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                                                                                                                                  diseases and cancer.
                                                      WPI; 2001-293287/31
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                  Holms RD;
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RESULT 2
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Sequence 8153, Appli
Sequence 8153, Ap
Sequence 14059, Ap
Sequence 144, Appli
Sequence 144, Appli
Sequence 144, Appli
Sequence 148, Appli
Sequence 148, Appli
Sequence 148, Appli
Sequence 148, Appli
Sequence 6, Appli
Sequence 16, Appli
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Sequence 16, Appli
Sequence 6, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      August 16, 2004, 09:54:23; Search time 39 Seconds (without alignments) 54.273 Million cell updates/sec
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Sequence 7,
Sequence 5,
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1 EREKEQMMREKEELMIRLQD.....BEKTKKAERELSEQIQRALQ
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6.
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-000C-6304
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                                                                                                                                                                                                                                                                                                                                                           389414 segs, 51625971 residues
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                                                                                    sw model
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                                                                                    using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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; Sequence 2, Application US/09040725A
; Patent No. 6399584
; GENERAL INFORMATION:
    APPLICANT: Institut Curie
; APPLICANT: Crepaldi, Tiziana
APPLICANT: Crepaldi, Tiziana
; APPLICANT: Generati, Alexis
APPLICANT: Crepaldi, Tiziana
; APPLICANT: Crepaldi, Tiziana
; APPLICANT: Crepaldi, Tiziana
; APPLICANT: Gautreau, Alexis
; APPLICANT: Louvard, Daniel
; TITLE OF INVENTION: on tyrosine 353
TITLE OF INVENTION: on tyrosine 353
FILE REFERRACE: 39108200100
; CURRENT APPLICATION NUMBER: US/09/040,725A
; UNMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                           GREARL INFORMATION:
APPLICANT: Institut Curie
APPLICANT: Arpin, Monique
APPLICANT: Crepaldi, Tiziana
APPLICANT: Crepaldi, Tiziana
APPLICANT: Crepaldi, Tiziana
APPLICANT: Crepaldi, Tiziana
APPLICANT: Guvard, Daniel
TITLE OF INVENTION: Parmaceutical composition containing ezrin mutated
TITLE OF INVENTION: On tyrosine 353
FILE REFERENCE: 39108200100
CURRENT APPLICATION NUMBER: US/09/040,725A
CURRENT FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 4
SSOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 586
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              Appl
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                                                Sequence 29, A Sequence 23, A Sequence 8, Ap Sequence 8, Ap Sequence 8, Ap Sequence 14, A Sequence 14, A Sequence 3, Ap
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              Sequence Sequence
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US-09-134-001C-3736
US-08-960-780-23
US-09-073-898-23
US-09-073-898-23
US-09-850-351A-23
US-09-850-351A-23
US-09-850-351A-29
US-08-53-351A-29
US-09-545-552-8
US-09-545-552-8
US-09-511-8338-14
US-09-971-8238-14
US-09-011-323-3
US-09-011-323-3
US-09-011-323-3
US-09-011-323-3
US-09-111-339-13
US-09-111-939-13
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                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09040725A Patent No. 6399584
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     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal
TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal
TITLE OF INVENTION: Adhesions and Uses Therefor
TITLE OF INVENTION: Adhesions and Uses Therefor
FILE REFERENCE: CSHL90-04FZA
CURRENT APPLICATION NUMBER: 103/09/848,294
CURRENT PILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 09/735,251
PRIOR APPLICATION NUMBER: 08/759,536
PRIOR PILING DATE: 1996-12-04
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR APPLICATION NUMBER: 07/663,579
PRIOR FILING DATE: 1991-03-01
PRIOR FILING DATE: 1991-03-01
PRIOR FILING DATE: 1990-03-14
NUMBER OF SEQ ID NOS: 13
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Fatent No. 5821091
GENERAL INPORATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 250 Cambridge Avenue, Suite 250
CITY: Palo Alto
STREET: GA
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 336;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 7; DB 4;
100.0%; Pred. No. 14;
tive 0; Mismatches
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NAME: Sholtz, Charles K.

RESERGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
                                                                                                                  RESULT 5
US-09-848-294-5
Sequence 5, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
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CLASSIFICATION: 435
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US-09-848-294-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 EREKEOM 336
                                    66 AERELSE 72
  28 AERELSE 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-05

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14059, Application US/09489039A
Patent No. 6610836
Patent No. 6610836
Patent No. 6610836
Patent No. CGLOBAD
Patent No. CGLOBAD
Patent No. CGLOBAD
Patent No. CGLOBAD
PAPLICATION:
APPLICATION:
APPLICATION:
NUMBER:
TITLE OF INVENTION:
PRICE PAPPLICATION NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT APPLICATION NUMBER: US/00-01-27
PRICE PAPLICATION NUMBER: US/00-01-27
PRICE PAPLICATION NUMBER: US/00-01-29
NUMBER OF SEQ ID NOS: 14342
NUMBER OF SEQ ID NOS: 14342
PARTOR 1272
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               SEQ ID NO 2
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (22)
COHER INPORMATION: Xaa = tyrosine or a phosphorylated tyrosine
US-09-040-725A-2
                                                                                                                                                                                                                                                                 Query Match 24.4%; Score 10; DB 4; Length 27; Best Local Similarity 100.0%; Pred. No. 0.0016; Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 249;
. 11;
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17.1%; Score 7; DB 4
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3

1.09-543-681A-8153

2. Sequence 8153, Application US/09543681A

3. Patent No. 6605709
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Proteus mirabilis
US-09-543-681A-8153
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 100.0
Matches 7; Conservative
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US-09-489-039A-14059
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Gaps

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GENERAL INFORMATION:
APPLICANT: WARINAMN, ROBERTO
TITLE OF INVENTION: HUMAN HOMOLOGUE OF YEAST HELICASE AND USES THEREOF
FILE REFERENCE: db7 sequence
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Sequence 144, Application US/09168595
Patent No. 655566
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 645;
                    Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/168,595
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100.0%; Pred. No. 24;
:ive 0; Mismatches
Pred. No. 24;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Sholtz. Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-011
TELECHONIC (A15) 324-0860
INFORMATION: (415) 324-0860
INFORMATION FOR SEQ ID NO. 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,126
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Patent No. 6518052
Best Local Similarity 100.0%; P
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; INDIVIDUAL ISOLATE: G18.pep
US-09-168-595-144
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Best Local Similarity 100.
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                                                                                                         483 KAERELS 489
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94306
                                                                                                                                                                       RESULT 8
US-09-168-595-144
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Pa
STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-425-335-2
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US-08-687-080-47
US-08-687-080
Specification US/08687080
Patent No. 5965427
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                  Length 645;
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                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC Compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC compatible
COMPUTER: Tab PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSFEICATION: AJS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 4600-0111.30
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                               Score 7; DB 2; Pred. No. 24; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                             17.1%; Sco.
100.0%; Pre
                    TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INPORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
// INDIVIDUAL ISOLATE: G18.pep
                                                                                                                                                                                                                                                                          ; INDIVIDUAL ISOLATE: G18.pep
US-08-592-126-144
  TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 645 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                               Query Match 17.1
Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                            CITY:
STATE:
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; Sequence 148, Application US/08592126
; Patent No. 5821031
; GENERAL INFORMATION:
    APPLICANT: Gregory Dolganov
    TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
    TITLE OF INVENTION: Polypeptides
    NUMBER OF SEQUENCES: 151
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Deblinger & Associates
    STREET: 350 Cambridge Avenue, Suite 250
    CITY: Palo Alto
    CITY: Palo Alto
    COUNTRY: USA
                                                                                                                                                                                                                                              .
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INDIVIDUAL ISOLATE: Rad50.pro-translation of SEQ ID NO:54
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                                                                                                                                                                                                   DB 4; Length 689; . 26;
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ABDIUM TYPE: Floppy disk
COMPUTER: BAPE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.1%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 45; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                       17.1%; Score 7; DB 4
100.0%; Pred. No. 26;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz. Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEFENDE: (415) 324-0860
TELEFENDE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 148:
CURRENT APPLICATION NUMBER: US/09/425,335
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 2
LENGTH: 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
                                                                                                                                                                                                       Query Match 17.1
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                      13 ELMLRLQ 19
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                                                                                                                           ; TYPE: PRT
; ORGANISM: HUMAN
US-09-425-335-2
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RESULT 11 US-08-687-080-51

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Sequence 51, Application US/08697080

Patent No. 5965427

GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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Sequence 148, Application US/09168595

Patent No. 6555666

GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANS. OF RAD50 cDNA (SEQ. 54), NT.
389 TO 4324
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                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
APPLICATION NATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholts, Charles K:
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELERPATION SEQUENCE TOWNER: 413 324-0960
INPORMATION FOR SEQ ID NO: 51: SEQUENCE TOWNER: 41312 amino acids
TWORNER: AND ACTURE SET TOWNER: 41312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.1%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TR
INDIVIDUAL ISOLATE: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1312 amino ac
TYPE: amino acid
STRANDEDNESS: single
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DB 2;
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CALLY 10154
MADIUM TYPE: FLOPPY DISK
MADIUM TYPE: FLOPPY DISK
COMPUTER: ISM PC COMPATIBLE
CORPUTER: ISM PC COMPATIBLE
CORRATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: ASCII
CURRARY APPLICATION DATA:
APPLICATION NUMBER: US/08/725,027
FILING DATE: 02-0CT-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,556
ATTORNEY/AGENT INFORMATION:
NAME: KATHRYN M. BROWN
REGISTRATION NUMBER: 34,556
REBRENCE/DOCKET NUMBER: 2026-4201US1
TELEPRANCE (212) 758-4800
TELEPRANCE (212) 758-4800
TELEPRANCE (212) 758-4800
TELEPRANCE (212) 751-6849
INFORMATION FOR SEQ ID NO: 6:
SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.6%; Score 6; DB 3
100.0%; Pred. No. 7.5
tive 0; Mismatches
                                                                                                                                                         14.6%; Score 6; DB 2
100.0%; Pred. No. 7.5
tive 0; Mismatches
                                                                                                                                              Query Match
Best Local Similarity 100.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino Acid
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Best Local Similarity 100.
Matches 6; Conservative
SEQUENCE CHARACTERISTICS:
                                      TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-08-725-027-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linear
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                                                                                                                       US-08-538-711A-6
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US-08-725-027-6
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APPLICANT: MULIANINE, JAMES, L.
APPLICANT: MULIANINE, JAMES, L.
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
NUMBER OF SEQUENCES:
ADDRESSES: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/168,595
FILING DATE: CLASSIFICATION
PRIOR APPLICATION NUMBER: 08/592,126
FILING DATE: NEPRORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (415) 324-0860
TELEFERAL (415) 324-0960
TELEFERAL (415) 324-0960
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.1%; Score 7; DB 4;
100.0%; Pred. No. 45;
vative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INPORMATION:
NAME: KATHRYN M. BROWN
REGISTATION UNDER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4201
TELECOMMUNICATION INFORMATION:
TELEFRONE: (212) 758-4800
TELEFRX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTINE SALASINE SORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/538,711A
FILING DATE: 0.2-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: CALCATION DATA:
APPLICATION NUMBER:
FILING DATE: CALCATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08538711A Patent No. 5994062
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 KAERELS 489
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STATE: NE
COUNTRY:
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US-08-538-711A-6
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Sequence 6, Application US/08725027
Patent No. 6251586
GENERAL INFORMATION:
APPLICANT: MULSHINE, JAMES, L.
APPLICANT: TOCKMAN, MELVYN, S.
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
NUMBER OF SEQUENCES: 23
CORRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                        0; Indels
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Length 12;
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US-09-542-552-6
; Sequence 6, Application US/09542552
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GENERAL INFORMATION:

APPLICANT WILSHINE, JAMES, L.

TITLE OF INVERNITON:

MUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE:

ADDRESSE:

ADDRESSE:

ADDRESSE:

ADDRESSE:

ADDRESSE:

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ADDRESSE:

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TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLGGY: Linear

MOLECULE TYPE: peptide

US-09-542-552-6
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Search completed: August 16, 2004, 09:57:43 Job time : 39 secs

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Gaps . 0

0; Indels

Page

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Mon Aug 16 10:46:50 2004
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August 16, 2004, 09:56:08; Search time 46 Seconds (without alignments) 279.805 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EREKEOMMREKEELMLRLQD......EEKTKKAERELSEGIORALQ 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1292805 segs, 313927144 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
                                                                                                                                              OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                             US-09-856-070B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
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				SUMMERES		
w	.% Query Score Match	-% Query Match Length DB	DB	ΙD	Description	
, 2	48.8	! ! !	14	US-10-106-698-4728	Seguence	4728, Ap
2	48.8	586	15	US-10-116-275-117	Sequence 117, App	117, App
~	48.8		16	US-10-408-765A-2372	Sequence 2372,	2372, Ap
ñ	48.8		16	US-10-408-765A-1160	Seguence 1160,	1160, Ap
Ñ	48.8		σ	US-09-925-299-896	Sequence 8	96, App
8			10	US-09-925-299-896	Seguence	896, App
ω,			12	US-09-988-493-8	Sequence	8, Appli
w			12	US-10-424-599-232000	Sequence 232000,	232000,
w			12	US-10-425-114-43920	Sequence 43920, A	43920, A
w			12	US-10-424-599-232005	Sequence	232005,
w			12	US-10-425-114-45766	Seguence	45766, A
w			12	US-10-424-599-232010	Sequence	232010,
w	8 19.5	391	12	US-10-424-599-232009	Sequence 232009,	232009,
w			12	US-10-425-114-55605	Seguence	55605, A
•	10 0		1	TR-10-425-114-56199	Segmence	56199. A

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Gaps 0

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aquence 5, A aguence 5, A aquence 43, aquence 59, aquence 34, aquence 24, aquence 11, aquence 11, aquence 11, aquence 6, equence 13, equence 6, equence 6, equence 13, equence 6, equence 13, equence 13, equence 6, equence 6, equence 13, equence	Sequence 53, Appl Sequence 226483,
US-10-424-599-22 US-09-848-224-5 US-10-108-294-214-5 US-10-108-2604-5 US-10-074-978A-108-10-074-978A-108-10-074-978A-108-10-074-978A-108-10-236-031B-108-10-236-238-11 US-09-976-2800A-24 US-09-976-2800A-24 US-10-438-077-28	US-09-933-780C-53 US-10-424-599-226483
4 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	11
	15 45
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11111 11111 11111 11111 11111 11111 1111	4 4 5 5

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Sequence 4728, Application US/10106698

Publication No. US20030109690A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

FILE REPERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR FILING DATE: 1999-09-29

PRIOR PLING DATE: 1999-10-3

PRIOR PLING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3.0

SEQ ID NO 4728

LENGTH: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC_FEATURE
LOCATION: (382)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%; Score 20; DB 14; Length 436;
.larity 100.0%; Pred. No. 2.1e-11;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 20; Conserv
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Gaps
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Sequence 896, Application US/09925299

Sequence 806, Application US/09925299

Patent No. US20020055627A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PALO2

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PATENTION PALE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SEQ ID NO 896

LENGTH: 635
                                                                    APPLICANT: Zhang, Bing
APPLICANT: Glbson, Bradford W.
APPLICANT: Glbson, Bradford W.
APPLICANT: Glenn, Cary W.
APPLICANT: Glenn, Cary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTECME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FREESE for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 630;
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Publication No. US20030040617A9;
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: PCT/US00/05883;
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
48.8%; Score 20; DB 16;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 20; Conservative 0; Mismatches 0.
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APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
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Matches 20; Conservative
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US-09-925-299-896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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US-09-925-299-896
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LENGTH: 630
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                                                                                       Sequence 117, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Blan Pharmaceutical Technology
APPLICANT: Drayden, David
APPLICANT: Brayden, David
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
APPLICANT: Compositions Targeting Peyer's Patches and M Cells and Methods and TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: B1067/20087
CURRENT APPLICANT: 2002-10-04
NUMBER OF SED ID NOS: 349
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| Publication No. US20040101874A1
| General Information |
| APPLICANT Ghosh, Soumitra S. |
| APPLICANT Ghosh, Bing |
| APPLICANT Giben, Gary M. |
| APPLICANT Giben, Gary M. |
| APPLICANT Glenn, Gary M. |
| APPLICANT Glenn, Cary M. |
| APPLICANT Glenn, Gary M. |
| APPLICANT Glenn, Gary M. |
| APPLICANT Warnock, Dale B. S. |
| TITLE OF INVENTION IDENTIFIED IN THE MITOCHONDRIAL PROTEOME FILING DATE: 2003-04-04 |
| VUMBER OF SEQ ID NOS: 3077 |
| SOUTHARE PARESE FRANCE 
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Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 20; Conservative 0; Mismatches 0;
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48.8%; Score 20; DB 15; I
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 20; Conservative 0; Mismatches 0;
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; Sequence 1160, Application US/10408765A
; Publication No. US20040101874A1
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SEQ ID NO 117
LENGTH: 586
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ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-10-116-275-117
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RESULT 3

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RESULT 4

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US-10-425-114-43920
US-10-425-114-43920
Sequence 43920, Application US/10425114
Sequence 43920, Application VS2004003488A1
Sequence 43920, Application No. US2004003488A1
Sequence 43920
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Covalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (5313) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 43920
LENTH: 170
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APPLICANT: Avail David K
APPLICANT: Cao Yongweith Titus
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 232005
LENGTH: 207
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                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_51518C.1.pep
US-10-424-599-232000
                                                                                                                                                                ore 8; DB 12;
red. No. 3;
Mismatches
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US-10-425-114-43920
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Pred. No.
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                                                                                                                                                                Query Match
Best Local Similarity 100.0%; P. Matches 8; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 TKKAEREL 32
                     TYPE: PRT ORGANISM: Glycine max FEATURE:
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LENGTH: 105
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Toou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICANTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 232000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/0988493
; Bublication No. US2003006441941
; GENERAL INFORMATION:
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Parekh, Rajesh Bhikhu
FILE REFERENCE: 2543-1-0.24
CURRENT APPLICATION UNMER: PG7/GB01/01219
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: GB 0007265.2
PRIOR APPLICATION NUMBER: GB 0007265.2
PRIOR APPLICATION NUMBER: 308
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 8
SEQ ID NO 8
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100.0%; Pred. No. c.
'''n 0; Mismatches
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100.0%; Pred. No. ...
0; Mismatches
PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1556 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 896 LENGTH: 635
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-09-925-299-896
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ORGANISM: homo sapien
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US-10-424-599-232000
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalid: David K
APPLICANT: Kovalid: David K
APPLICANT: Applicant: Son Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Number and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Number (33.13) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
SEQ ID NOS: 73128
LENGTH: 408
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Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches 0; Indels
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US-10-424-599-232009
                                                                                                                                                                  US-10-424-599-232009
; Sequence 232009, Application US/10424599
; Publication No. US20040031072A1
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Matches 8; Conservative
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                                                                      257 TKKAEREL 264
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                          25 TKKAEREL 32
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LENGTH: 391
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Sequence 45766, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: APPLICANT: ADAVIG K.
APPLICANT: Gao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

SEQ ID NO 45766

LENGTH: 207
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53223)
FILE REFERENCE: 38-21(53223)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 232010
LENGTH: 298
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19.5%; Score 8; DB 12; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels
  DB 12; Length 207; . 5.4;
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US-10-424-599-232010
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US-10-425-114-45766
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 100.0%; Pred. No. 5.4
Matches 8; Conservative 0; Mismatches
Query Match 19.5%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 5.4
Matches 8; Conservative 0; Mismatches
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US-10-425-114-45766
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US-10-425-114-56199
; Sequence 56199, Application US/10425114
; Publication No. US2040034888A1
; CRNERAL INPORMATION:
APPLICANT: Zhou, Yingdong
; APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei E
APPLICANT: Cao, Yongwei E
APPLICANT: Tabaska, Jack E
APPLICANT: Jack E
APPLICANT:
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Search completed: August 16, 2004, 10:02:25 Job time: 47 secs

368 TKKAEREL 375

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                                                                                       August 16, 2004, 09:53:32 ; Search time 38 Seconds (without alignments) 103.786 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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No.
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A3400
A3416 Auman
NyAlternate names: cytovillin; p81 protein; villin 2
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Accession: A34400; 509263; E61002
C;Accession: A34400; 509263; E61002
C;Accession: A34400; 509263; E61002
C;Accession: A34400; Mingrist, R.; Pakkanen, R.; Grzeschik, K.H.; Wahlstroem, T.; Vaheri, A.; Title: Cytovillin, a microvillar M-r 75,000 protein. cDNA sequence, prokaryotic express A;Title: Cytovillin, a microvillar M-r 75,000 protein. cDNA sequence, prokaryotic express A;Recession: A34400; MUD:89380299; PMID:2674140
A;Recession: A34400; MUD:89380299; PMID:2674140
A;Residues: 1-586 <TUR>
A;Residues: 1-586 <TUR>
A;Residues: 1-586 <TUR>
A;Note: the translation of residues 1-11 is not given
A;Note: parts of this sequence were confirmed by protein sequencing
R;Gorid, K.L.; Bretscher, A.; E8Ch, F.S.; Hunter, T.
EMBO J. 8, 4133-4142, 1989
A;Title: cNNA cloning and sequencing of the protein-tyrosine kinase substrate, ezrin, revented and sections of the protein-tyrosine kinase substrate, procession procession procession.

A;Molecule type: mRNA A;Residues: 2-586 <GOU> A;Cross-references: GB:X51521; NID:g31282; PIDN:CAA35893.1; PID:g31283

A; Accession: S09263

130 6 14.6 112 2 B86951 8151  32 6 14.6 116 2 B96951 Py  33 6 14.6 116 2 B96951 Py  34 6 14.6 1139 2 B56904 Py  35 6 14.6 139 2 B56904 Py  36 6 14.6 139 2 B56904 Py  37 6 14.6 139 2 B56904 Py  40 6 14.6 139 2 AB081 Py  41 6 14.6 153 2 T1571 Py  42 6 14.6 163 1 S01399 Py  43 6 14.6 163 2 B8040 Py  44 6 14.6 169 2 B8040 Py  45 6 14.6 190 2 G70239 Gy  46 6 14.6 190 2 G70239 Gy  47 6 14.6 190 2 G70239 Gy  48 6 14.6 190 2 G70239 Gy  49 6 14.6 190 2 G70239 Gy  40 6 14.6 190 2 B8040 Py  41 6 14.6 190 2 G70239 Gy  42 6 14.6 190 2 G70239 Gy  43 6 14.6 190 2 G70239 Gy  44 6 14.6 190 2 G70239 Gy  ALIGNMENTS  RESULT 1  ALIGNMENTS  ALI	transcription repr similar to arsenat hypotherical prote flagellar basal bo robable thioredoxi probable thioredox probable thioredox thioredoxin 2 [imp hypotherical prote hypotherical prote H+-transporting tw petp protein - Rho protein F47F6.4 [i ribosome recycling conserved hypother gene sj22 protein	MENTS	le) 15-Oct-1996 #text_change 24-Nov-2003 Duman, R.S.; Nestler, B.J. reins associated with cell shape and growth, are e	from GB/EMBL/DDBJ :9289407; PIDN:AAA30510.1; PID:9289408 n family; protein 4.1 membrane-binding domain homology ne-binding domain homology <b41></b41>	re 20; DB 2; Length 581; ed. No. 2.8e-12; Mismatches 0; Indels 0; Gaps 0;	
## 112 2	H82197 F90621 A704024 A704024 A704024 H991059 AB0831 F69160 S01399 S01399 G71725 G71725	ALIGNMENTS	s (cattle) rision 15-Oct 1, K.; Duman 993	d from GB, ID:928940' sin family rane-bind	Sco ; Pr	
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	0 E E E E E E E E E E E E E E E E E E E	RESULT 1 145889 ezrin -	C;Specie C;Date: C;Access R;Bergsc Mol: Cel A;Title: A;Refere	A; Molecu A; Molecu A; Residu A; Cross- C; Superf F; 7-291/	Query Best I Matche	yy qa

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A, Accession: B46501
A, Status: preliminary
A, Status: preliminary
A, Residues: 53-57,148'L',150',G',152-155 < EG3>
A, Experimental source: MRL lpr/lpr, T-cells
A, Experimental source: MRL lpr/lpr, T-cells
A, Experimental source: MRL pr/lpr, T-cells
A, Mote: sequence extracted from NCBI backbone (NCBIP:112940)
C, Comment: This protein is located in microvilli and is proposed to play a role in module C, Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology
C, Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-associated protein; phosphoprome P, 2-586/Product: ezrin #status predicted < MAT>
F, 7-291/Domain: protein 4.1 membrane-binding domain homology < E81>
F, 7-953-586/Region: actin binding #status predicted
F, 66/Binding site: phosphate (Ser) (covalent) #status predicted
F, 299, 332/Binding site: phosphate (Thr) (covalent) #status predicted
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(17.3K hypothetical protein F28823.5 - Arabidopsis thaliana
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Orabar, Marcoll #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
(Species: Orabar, M.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Chung, M.; Conny, L.; Conny, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

Nature 408, 816-820, 200
(A.; Hughes, B.; Huizar, J., Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A.Authors: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Reference number: A86141; MUID:21016719; PMID:11130712
A;Cross-references: EMBL:X60671; NID:950880; PIDN:CAA43086.1; PID:950881
R;Egerton, M.; Burgess, W.H.; Chen, D.; Druker, B.J.; Bretscher, A.; Samelson, L.E.
J. Immunol. 149, 1847-1852, 1992
A;Title: Identification of exrin as an 81-kDa tyrosine-phosphorylated protein in T cells.
A;Reference number: A46501; MUID:92388649; PMID:1381389
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A;Residues: 1-142 <STO>
A;Cross-references: GB:AE005172; NID:g11079495; PIDN:AAG29206.1; GSPDB:GN00141
C;Genetics:
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Pred. No. 0.00026;
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A;Status: preliminary
A;Molecule: type: protein
A;Espatimenta: 27-33,E' < EG2>
A;Experimental source: MRL lpr/lpr, T-cells
A;Note: sequence extracted from NCBI backbone (NCBIP:112936)
                                                                                                                                                                                                                                                                                                                                    A;Experimental source: MRL lpr/lpr, T-cells
A;Note: sequence_extracted from NCBI backbone (NCBIP:112938)
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                                                                                                                                                                                                                                      A,Status: preliminary
A,Molecule type: protein
A,Residues: 412-426 <EGE>
A,Experimental source: MRL
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les 7; Conserv
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                                                                                                                                                                                                   A;Accession: C46501
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               O
           R;Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; C Blectrophoresis 11, 528-536, 1990
Bjectrophoresis 11, 528-536, 1990
A;Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencin A;Reference number: A61002; MUID:91031404; PMID:1699755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Map position: 6q25-6q26
(Superfamily: ezrin/radixin/moesin family, protein 4.1 membrane-binding domain homology
(Superfamily: ezrin/radixin/moesin family, protein 4.1 membrane-binding
(SKeywords actin binding, cytoskeleton; membrane-associated protein; phosphoprotein
F;2-586/Product: ezrin #status experimental <MAT>
F;7-291/Domain: protein 4.1 membrane-binding domain homology <841>
F;553-586/Region: actin binding #status predicted
F;66/Binding site: phosphate (Ser) (covalent) #status predicted
F;214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted
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;Superfamily: ezrin/radixin/moesin family; protein 4.1 membrane-binding domain homology
                                                                                                                                                                                                   A,Molecule type: protein
A,Residues: 255-263;194,'Q',196-199,'X',201;264-270 <BAU>
A;Residues: 255-263;194,'Q',196-199,'X',201;264-270 <BAU>
A;Note: it is not certain whether this material represents ezrin or radixin (see entry P A;Note: this material corresponds to transformed epithelial amnion cell (AMA) database C;Comment: This protein is located in microvilli and is proposed to play a role in modul C;Genetics:
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Cibate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 24-Nov-2003
Cibate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 24-Nov-2003
Cibate: 20-Apr-2000 #sequence_revision 20-Apr-2000
Cibatesion: T47177
Aistatus: preliminary
Aisolecule type: mRNA
Aistatus: preliminary
Aisolecule type: mRNA
Aistatus: 1-630 cAAA>Aistatus: BMBL:AL162086
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Aug-1992 #sequence revision 14-Jul-1994 #text_change 24-Nov-2003
C;Accession: B41129; C46501; A46501; B46501; S24200
R;Funayama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.; Tsukita, S.
A;Title: Radixin is a novel member of the band 4.1 family.
A;Reference number: A41129; MUD:92064635; PMID:1955455
A;Accession: B41129
A;Residues: 1-586 <FUN>
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A,Note: DKFZp762H157,1
C,Superfamily: ezrin/Fadixin/moesin family; protein 4.1 membrane-binding dc
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48.8%; Score 20; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
Matches 20; Conserv
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A; Cross-reference
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Best Local Similarity 100.
Matches 7; Conservative
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A, Molecule type: DNA
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Matches
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                                                                            C, Function:
A, Description: represses transcription of at least eight genes required for fatty acid the biosynthesis, activates the iclR gene encoding the transcription regulator of the aceBAK A, Pathway: fatty acid metabolism
A, Pathway: fatty acid metabolism
A, Note: fadR-dependent DNA binding and transcriptional activation is prevented by long of
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Nucleic Acids Res. 16, 7995-8009, 1988
A.fitle: Nucleotide sequence of the fadR gene, a multifunctional regulator of fatty acid
A.Reference number: S01288; MUID:88335542; PMID:2843809
A.Accession: S01288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Residues: 1146,Tr,148-239 <DIR>
A)Cross-references: RNBL:X08087; NID:g992990; PID:g992991
A)Cross-references: RNBL:X08087; NID:g992990; PID:g992991
A)Experimental source: strain K-12
A)Note: the author translated the codon ACC for residue 147 as Asn
R;DiRusso, C.C.; Helmert, T.L.; Netzger, A.K.
J; BAOl. Chem. 267, 8685-8691, 1992
A;Title: Characterization of FadR, a global transcriptional regulator of fatty acid meta
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-239 <BLAT>
A;Cross-references: GB:AE000217; GB:U00096; NID:g1787434; PIDN:AAC74271.1; PID:g1787436;
A;Experimental source: strain K-12; substrain MG1655
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A;Accession: AF0261
A;Status: preliminary
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C;Keywords: DNA binding; homodimer; transcription regulation
F;31-55/Region: helix-turn-helix motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Reference number: A38103, MUID:92235103, PMID:1569108
A,Accession: A38103
A,Status: preliminary
A,Molecule type: protein
A,Residues: 2-11 < Diz>
C,Genetics:
A,Gene: fadR; oleR; thdB
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100.0%; Pred. No. 12;
cive 0; Mismatches
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Best Local Similarity 100.0
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DNA-binding protein, fatty acid/fatty acyl-responsive - Escherichia coli (strain O157:H7, C). Species: Bacherichia coli
C; Accession: B99839
D; A; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Saswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
DNA Res. 9, 11-22, 2001
D; Reference number: A99629; MUID:21156231; PMID:11258796
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-239 <AAX
A; Residues: 1-239 <AAX
A; Resperimental source: strain O157:H7, substrain RIMD 0509952
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A;Residues: 1-239 <270>
A;Cross-references: GB:AE005174; NID:g12514884; PIDN:AAG56038.1; GSPDB:GN00145; UWGP:Z19!
A;Experimental source: strain O157:H7, substrain EDL933
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Bs6697
B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409; S29-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Accession: B85697
A;Status: preliminary
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A; Residues: 1-239 < XUR>
A; Residues: 1-239 < XUR>
A; Cross-references: GB:AL590842; PIDN:CAC90954.1; PID:g15980150; GSPDB:GN00175 C; Genetics: A; Genetics: A; Genetics: fadR C; Superfamily: pyruvate dehydrogenase complex repressor
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C;Guperfamily: pyruvate dehydrogenase complex repressor
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Local Similarity 100.0%; Pred. No. 12;
tes 7; Conservative 0; Mismatches
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100.0%; Pred. No. 12;
cive 0; Mismatches
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33 AERELSE 39

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RESULT 10

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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-b Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homoserine kinase (thrB) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: 690407 R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-P. R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-P. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
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Ribrack, Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
Ribrack, Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
A;Reference number: Z21884
A;Reference number: Z21884
A;Scession: T40769
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: 1-452 CMN>
A;Residues: 1-452 CMN>
A;Cross-references: EMIN-AA,C1837; PIDN:CAA,7041.1; GSPDB:GN00067; SPDB:SPBC947.13
A;Experimental source: strain 972h-; cosmid c947
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A;Reaidues: 1-303 <KUR>
A;Cross-references: GB:AE006641; NID:g13816366; PIDN:AAK43085.1; GSFDB:GN00155
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-311 <KUR>
A;Cross-references: GB:AE006641; NID:g13815670; PIDN:AAK42518.1; GSPDB:GN00155
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100.0%; Pred. No. 15;
tive 0; Mismatches
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C, Superfamily: homoserine kinase
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Best Local Similarity 100.0
Matches 7; Conservative
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A;Accession: G90407
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A;Gene: SPDB:SPBC947.13
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A;Status: preliminary
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Nature 406, 477-483, 2000
A,771tle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A,Reference number: A82035, MUD:20406833; PMID:10952301
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-279 cHEI>
A,Residues: 1-279 cHEI>
A,Cross-references: GB:AE003852, NID:g9656424; PIDN:AAF95048.1; GSPDB:GN001
A,Experimental source: serogroup 01, strain NI6961; biotype El Tor
                                                                                                                                                                                              fatty acid-fatty acyl responsive DNA-binding protein [imported] - Salmonella enterica su
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0723
                                                                                                                                                                                                                                                                                                                                                                                 R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Asture 413, 848-852, 2001
A; Athebors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; MUID:21534947; PMID:11677608
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A;Molecule type: DNA
A;Residues: 1-239 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05488.1; PID:g16502992; GSPDB:GN00176
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A;Gene: STY1934 C;Superfamily: pyruvate dehydrogenase complex repressor

C;Genetics:

A; Accession: AF0723

33 AERELSE 39

RESULT 11

28 AERELSE 34

C;Genetics: A;Gene: VC1900 A;Map position: 1 C;Superfamily: pyruvate dehydrogenase complex repressor

Query Match
Best Local Similarity 100.
Matches 7; Conservative

28 AERELSE 34 AERELSE 39

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RESULT 12 F90478

Pred. No. 20;

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A, Status: preliminary
A, Moccession: S66049
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-563 - COGA-
A, Enris, Browning, C. B. Bruschi, C. V.; Caddwall, B.; Capuano, V.; Carter, N.M.; Choracter, S. Broulliet, S. Bruschi, C. V.; Caddwall, B.; Capuano, V.; Carter, N.M.; Choracter, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G.; Krogh, S.; Roche, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauch, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle Raeger, M.; Rivolta, C.; Roche, B.; Roche, M.; Sadaie, Y.; Sato, T.; Scanlon, A, Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekfuguchi, J.; Sekowska, A.; Johnitors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekfuguchi, J.; Sekowska, A.; Johnitors: Schleich, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Vohiyama, A, Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A, Schroets: Palaninary; nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
A, Rochester. 1-643 - KNNA
A, Rochester. 1-643 - KNNA
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313766
DNA-directed DNA polymerase (EC 2.7.7.7) III chain dnaX - Bacillus subtilis
DNA-directed DNA polymerase (IC 2.7.7.7) III chain dnaX - Bacillus subtilis
Cispecies: Cispecies: Solovis; Seforas and 19-May-1994 #text_change 20-Jun-2000
Cispecies: Sintahige, K.; Ogasawara, N.
Nucleic Acids Res. 18, 671-677, 1990
A;Title: Molecular cloning, genetic characterization and DNA sequence analysis of the represence number: S13786; MUID:91088245; PMID:2124672
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A; Residues: 1-563 <ALLO.
A; Cross-references: ENBL:X17014; NID:9453238; PIDN:CAA34877.1; PID:9580914
A; Cross-references: ENBL:X17014; NID:9453238; PIDN:CAA34877.1; PID:9580914
R; Struck, J.C.R.; Vogel, D.W.; Ulbrich, N.; Erdmann, V.A.
R; Struck, J.C.R.; Vogel, D.W.; Ulbrich, N.; Erdmann, V.A.
A; Struck, J.C.R.; Vogel, D.W.; Ulbrich, N.; Erdmann, V.A.
A; Title: A data A and A 
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A Residues: 1-422 <STR>
A;Cross-references: HMBL:X06803; NID:g39891; PIDN:CAA29958.1; PID:g580855
R;Cgasawara, N.; Nakai, S.; Yoshikawa, H.
B;Cgasawara, I. 1-14 1994
A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom
A;Reference number: S65967; MUID:96051385; PMID:7584024
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A;Experimental source: strain 168
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A;Start codon: GTG
C;Superfamily: DNA-directed DNA polymerase III gamma chain
C;Keywords: nucleotidyltransferase
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100.0%; Pred. No. 25;
tive 0; Mismatches
                                                                  Mismatches
Best Local Similarity 100.0%; P. Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                      122 KKAEREL 128
                                                                                                                                                                                           26 KKAEREL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-563 <KUN>
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315 RELSEQI 321

completed: August 16, 2004, 09:56:52 ne : 38 secs

30 RELSEQI 36

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thermoanaer bacillus ca methanobact bacillus ps rhodobacter

067244 P33636 Q8rb52 P41014 Q50521 P09221

escherichia

bordetella bordetella bordetella rickettsia

07wqs9 H 07w1v3 H 07vs88 H 09ze08 H

escherichia

us-09-856-070b-29.0li.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Kidney;
MEDLINE-96239137; PubMed-8660651;
MEDLINE-96239137; PubMed-8660651;
Galat A., Garbod M.C., Bouet F., Riviere S.;
and applications.";
Arch. Blochem. Blophys. 330:229-237(1996).
-!-FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-!-SUBCELIULAR LOCATION: Microvillar peripheral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bergson C.M., Zhao H., Saijoh K., Duman R.S., Nestler E.J.;
"Ezzin and osteonectin, two proteins associated with cell shape and
growth, are enriched in the locus coeruleus.";
                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Rikaryota: Metazoa; Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (cytoplasmic side).

(rytoplasmic side).

- PTM: Phosphorylated by tyrosine-protein kinases.

- SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2093 (Rel. 42, Last annotation update)
Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                      ALIGNMENTS
FLGB_AQUAE
1912_ECOLI
1972_THEIN
ATPF_BACCA
1848_METTW
ATPF_BACP3
PETP_RHOCA
DEFT_BORPA
DEFT_BORPA
DEFT_BORPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M98498; AAA30510.1; -.
PIR; 14589; 14589.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000299; Ex/rad/moesin.
InterPro; IPR000998; Ex/rad/moesin.
Pfam; PF00759; EMM_1; 1.
Pfam; PF00769; EMM_1; 1.
PRNRT; SM00295; BAND41.
SMART; SM00295; BAL; 1.
PROSITE; PS00660; PERM_1; 1.
PROSITE; PS00660; PERM_2; 1.
                                                                                                                                                        RICPR
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                                                                                                                                                                       PAAY
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                                                                                                                                                                                                                                                                                                     STANDARD;
   SEQUENCE FROM N.A.
TISSUE=Brain;
   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                    EZRI BOVIN
ID EZRI BOVIN
AC P31976;
   RESULT 1
     459789017844
459786017845
                                                                                                                                                                                                                                                                                                          sus scrofa
rattus norv
gallus gall
homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo sapien
mus musculu
escherichia
salmonella
salmonella
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shewanella
vibrio chol
vibrio para
vibrio vulu
sulfolobus
bacillus su
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homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                              August 16, 2004, 09:52:02; Search time 32 Seconds (without alignments) 66.715 Million cell updates/sec
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41
1 EREKEÇMMREKEELMLRLQD.......EEKTKKAERELSEQIQRALQ 41
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Q8ze19
Q8dqu8
Q8dqu8
Q8dqu9
Q8dqu9
Q8dqu9
Q9102
P26041
P26042
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Q34419
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                       141681 segs, 52070155 residues
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FADR SHEON
PADR VIBPA
FADR VIBPA
FADR VIBPO
KHSE SULSO
MOES HUMAN
MOES HUMAN
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MORES_RAIC
RADI_CHICKAN
RADI_HOUSE
RADI_HOUSE
RADI_PIG
EVC MOUSE
RADI_RAIT
BUC MOUSE
RADI_RAIT
BUC MOUSE
ROM
SCHOO
RALII RAT
HDA6_HUMAN
V311_TREPA
CH10_STRUI
CYTS_PIG
CYTS_PIG
RSR1_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EZRI BOVIN
EZRI HUMAN
EZRI MOUSE
FADR ECOLI
FADR SALTI
                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length
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Perfect 8
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MEDILINE-22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.R., Zeeberg B., Buerow K.H., Schemen C.M., Schuler G.D.,
Altschul S.R., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
Altschul S.R., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
A Hopkins R.F., Jordan H., Moore T., Max, Rubin G.M., Hong L.,
Stapleron M.J., Soares M.B., Soanaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
B Brownstein M.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
A Raha S.S., Loquellano N.A., Peters G.J., Abzamson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Wilting M., Madan A., Young A.C., Shevotenko Y., Bouffard G.G.,
A Blakesley R.W. Touchman J.W. Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
B Lterfield Y.S.N., Krzywinski M.I., Skaalska U., Smailus D.E.,
B Chenerch A., Schein J.E., Jones S.J.M., Marra M.A.,
R Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
MEDLINE=89380299; PubMed=2674140;
Turunen O., Winqvist R., Pakkanen R., Grzeschik K.-H., Wahlstroem T.,
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANT LEU-531.
Ottenwaelder B., Obermaier B., Mewes H.-W., Weil B., Wiemann S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDILINE=90076135; Pubmed=2591371;
GOULD K.L., Bretscher A., Esch F.S., Hunter T.;
"CDNA cloning and sequencing of the protein-tyrosine kinase substrate, ezrin, reveals homology to band 4.1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaheri A.;
"Cytovillin, a microvillar Mr 75,000 protein. cDNA sequence,
"Cytovillin, a microvillar Mr 75,000 protein. cDNA sequence,
"Prokaryotic expression, and chromosomal localization.";
J. Biol. Chem. 264:16727-16732(1989)
                                                                                                                                                                                                                                                                                                   48.8%; Score 20; DB 1; Length 580; 100.0%; Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                               PHOSPHORYLATION (BY PDGFR) (BY SIMILARITY). PHOSPHORYLATION (BY PDGFR)
                                                                                                                                                                                                   (BY SIMILARITY).
ECD663E5C200FAA3 CRC64;
Structural protein; Cytoskeleton; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EZRI HUMAN STANDARD; PRT; 585 AA. P1531; P23714; Q96CU8; Q9NSJ4; 01-APR-1990 (Rel. 14, Created) 01-NOV-1991 (Rel. 20, Last sequence update) COCT-2003 (Rel. 42, Last annotation update) Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                           100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EREKEQMMREKEELMLRLQD 20
                                                                                                                                                                                                                                      580 AA; 68629 MW;
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                                                               294
145
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es 20; Conserv
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145
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DOMAIN
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Matches
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       STTTTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of ezrin as an 81-kDa tyrosine-phosphorylated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Immunol. 149:1847-1852(1992).
-!- FUNCTION: Probably involved in connections of major cytoskeletal structures to the plasma membrane.
-!- SUBCELLULAR LOCATION: Microvillar peripheral membrane protein
                                                                                                           MEDLINE=96311348; PubMed=8713105; Sepercon M., Moritz R.J., Druker B., Kelso A., Simpson R.J.; Identification of the 70kD heat shock cognate protein (Hsc70) and alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (cytoplasmic side).
-!- TISSUE SPECIFICITY: Component of the microvilli of intestinal epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                          Krieg J., Hunter T.;
"Identification of the two major epidermal growth factor-induced
tyrosine phosphorylation sites in the microvillar core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural protein; CyToskeleton; Phosphorylation; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=9238649; PubMed=1381389;
Egerton M., Burgess W.H., Chen D., Druker B.J., Bretscher A.,
Samelson L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY PDGFR)
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2A844D140E3B06CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PTM: Phosphorylated by tyrosine-protein kinases.
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 224:666-674(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ein.";
Biol. Chem. 267:19258-19265(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; JOS021; AAA61278.1; ALT INIT.
EMBL; AL162086; CAB82418.1; ALT_INIT.
EMBL; BC013903; AAH13903.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000299; Band 4.1.
Interpro; IPR000798; Ez/rad/moesin.
Interpro; IPR008954; Messin.
Pfam; PF00373; Band 41; 1.
Pfam; PF00769; ERM; 1.
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                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92406868; PubMed=1382070;
                                                                                     SEQUENCE OF 171-179 AND 342-349
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SWART; SM00295; B41; 1.
PROSITE; PS00660; FERM_1; 1.
PROSITE; PS00661; FERM_2; 1.
PROSITE; PS50057; FERM_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X51521; CAA35893.1; -.
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PDB; 1NI2; 25-FEB-03.
SWISS-2DPAGE; P15311; HUMAN.
                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION BY PDGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:12691; VIL2.
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DB 1; Length 585;

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AN INELINE-22346483; FUDNGG-12466851;
AN INKAIGO I., OSATON N., SAITOR., SUZUKİ H., YAMADAĞA I., KİYOSAWA H.,
ANIKAIĞO I., OSATON N., SAITOR., SUZUKİ H., YAMADAĞA I., KİYOSAWA H.,
ANIKAIĞO I., OSATON N., SAITOR Y., HONDAĞA I., SCHÖNDAĞA C., GÖJÖDDOTI I.,
AN BAİAKA J.A., BYAĞI D., BYLUSI C., HONDAĞA C., GÖJÖDDOTI I.,
AN BAİAKA J.A., BYAĞI D., BYLUSI V., CHOCHIA C., COTADII U.E., COUSINS S.,
AN DALIA E., DYAĞARIDI T.A., Fletcher C.F., FOTTEST R., FOTTER K.N.,
AN GASTERINGING N., HITOKAWA N., JÖCKSON I.J., JARVİS B.D.,
AN AMADA A., KAVOCHKİN I.V., IEE Y., LEHDAĞA B.L.,
ANGAĞA A., KUTOCHKİN I.V., IEE Y., LEHDAĞA B.L.,
ANGAĞALIMA T., NUMMETA K., OKİĞO T., PATRAĞA B.L.,
ANGAĞALIMA T., NUMMETA M., MACHIDIN D., NARMAĞALIMA B.,
ANGAĞABİ M., SCHNEĞA T., REĞĞA D.J., PETRAĞA G., PESOLE G.,
ANGAĞA B., SALADA Y., KAĞABİ M.,
AN ANGAĞA M., SİLMAĞA K.,
ANDAĞA SALADA M., SİLMAĞA K.,
ANDAĞA M., MANDAŞA M., SALADA M., SALADA E.,
ANDAĞA M., MANDAŞA M., MANDAŞA M., YANG I., YANG I.,
ANDAĞA M., HASHİZAMA T., KONDO H., NARAWA T., FUKUĞA S.,
ANDAĞA M., HASHİZAMA T., KONDO H., NARAWA T., FUKUĞA S.,
ANDAĞA M., HASHİZAMA T., KONDO H., NARAWA T., FUKUĞA S.,
ANDAĞA M., HASHİZAME M., INOTANI K., ISHİİ Y., ICCH M., KAĞAWA I.,
ANDAĞA M., HASHİZAME M., MANDAĞA M., ANAMAMA A.,
ANIMAZAKİ T., WASHİXA, M., MARAMA T., KAĞAWA T., FUKUĞA S.,
ANIMAZAKİ A., SƏRAMİ M., MANDA M., SHİNDAĞA M.,
ANIMAZAKİ A., SƏRAMİ M., MANDA M., SHİNDAĞA M.,
ANIMAZAKİ A., SƏRAMİ M., MANDA M., SHİNDAĞA M.,
ANIMAZAKİ A., SƏRAMİ M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., MANDA M., 
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"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
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STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Fehigold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buercw K.H., Schemer C.M., Schuler G.D.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Vodin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-22064635; PubMed=1955455;
Funayama N., Nagafuchi A., Sato N., Tsukita S.;
"Radixin is a novel member of the band 4.1 family.";
J. Cell Biol. 115:1039-1048(1991).
                                             Indels
            Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                EZRI_MOUSE STANDARD; PRT; 585 AA. P26040; Q80ZT8; Q9DCI1; C1-MAY-1992 (Rel. 22, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-DCT-2004 (Rel. 43, Last amnotation update) Ezrin (p81) (Cytovillin) (Villin 2).
                                             Mismatches
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STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                        333 EREKEÇMMREKEBLMLRLQD 352
                                                                                                                          1 EREKEOMMREKEELMLRLOD 20
                                             0;
            100.08;
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                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (Mouse)
            Best Local Similarity
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                                                     Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P09371; P76827; D178727; D178727; D178727; D178727; D178727; D178727; D178727; D178727; D178727; D178727; D178727; D178727; D178727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D179727; D1797
                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Probably involved in connections of major cytoskeletal
structures to the plasma membrane.
-!- SUBCELMUAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Component of the microvilli of intestinal
epithelial cells.
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T -> A (IN REF. 1).

Q -> R (IN REF. 2).

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BY SIMILARITY.
FERM.
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EMBL; AK002766; BAB2341.1; -.
EMBL; BC048181; AA448181.2; -.
PIR; B41129; B41129.
MGD; MAI:98931, V412.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000799; Bald 4.1.
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SMART, SM00295, B41; 1.
PROSITE; PS00060; FERM_1; 1.
PROSITE; PS00061; FERM_2; 1.
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Pfam; PF00769; ERM; 1.
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FADR ECOLI
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SPECIES=E.coli, STRAIN=K12;
SPECIES=E.coli, STRAIN=K12;
SPECIES=E.coli, STRAIN=K12;
SPECIES=E.coli, STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihaza M., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihaza M., Mashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Misobuchi K.,
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Mori H., Motomura K., Nakamura Y., Nashimoto H., Wada C., Yamamoto Y.,
Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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SPECIESE.C.O.O.1; STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
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SPECIESE..coli; STRAIN=06;H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
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Mayhaw H.T., Donnamberg M.S., Blattner F.R.,
"Extensive mosaic_structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=KI2 / MG1655, SPECIESE=S.coli; STRAIN=KI2 / MG1655, MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Klaby M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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Nature 409:529-533(2001).
                                                                   Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
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Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yon G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
                                                                                   Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12;
MEDLINE=88335542; PubMed=2843809;
Escherichia coli 06,
Escherichia coli 0157:H7, and
Shigella flexneri.
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MEDIANE-2124500; PubMed=11279025;

X. Ray CRYSTALLOGRAPHY (1.5 ANGSTROMS).

X. W. Heath R.J., Li Z., Rock C.O., White S.W.;

X. W. Heath R.J., Li Z., Rock C.O., White S.W.;

The FadR. DNA complex. Transcriptional control of fatty acid
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J. Biol. Chem. 276:17373-17379 (2001).

Represses transcription of at least eight genes required for fatty acid transport and beta-oxidation among which fadA, fadB, fadD, fadL and fadB. Activates transcription of at least three genes required for unsaturated fatty acid biosynthesis: fabA, fabB and iclR, the gene encoding the transcriptional regulator of the aceBAK operon encoding the sylvaxlate shunt enzymes. Binding of fadR is specifically inhibited by long chain fatty acyl-CoA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157.", Nucleic Acids Res. 30:4432-4441(2002),
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Shen J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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"The structural basis of acyl coenzyme A-dependent regulation of the
                       comparison with a laboratory strain K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T.";
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-!- SUBCELLUIAR LOCATION: Cytoplasmic (Potential).
-!- DOMAIN: The C-terminal domain bind acyl-CoA.
-!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
"Complete genome sequence of enterohemorrhagic Escherichia
                                                                                          PARTIAL SEQUENCE, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
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J. Biol. Chem. 272:30645-30650(1997)
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MEDLINE=92235103; PubMed=1569108;
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EMBO J. 20:2041-2050(2001).
                     0157:H7 and genomic com
DNA Res. 8:11-22(2001).
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CHARACTERIZATION.
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Nature 413:848-852(2001).
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HAMAP: MF 00696; -; 1.

InterPro; IPR00820; FadR C.

InterPro; IPR00524; HTH GntR.

PRINTS; PR00395; HTHGNTR.

SMART; SM00345; HTHGNTR. 1.

PROSTIT; PS00043; HTH GNTR. 1.

PROSTIT; PS00043; HTH GNTR. PAMILY; 1.

PROSTIT; PG0043; HTH GNTR. PAMILY; 1.

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Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Fatty acid metabolism regulator protein.
Sabm ON STY1934 OR T1072.
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EMBL, AE005335; AAG56038.1; --
EMBL, AE002555; BAB35105.1; --
EMBL, AE015344; AAN42791.1; ALT_INIT.
EMBL, AE015982; AAP16682.1; --
FIR, B99839; B99839.
FIR, H64864; H64864.
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EMBL; AAC74271.1; -.
EMBL; D90753; BAA36042.1; -.
EMBL; D90752; BAA36034.1; -.
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; 1HW1; 06-JUN-01.
; 1HW2; 04-JUN-01.
Gene; EG10281; fadR.
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PROSITE; PS00043; HTH GNTR FAMILY; 1.
Fatty acid metabolism; Transcription regulation; Activator; Repressor;
DNA-binding; Complete proteome.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Fatty acid metabolism regulator protein.
FapR OR STM1805.
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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33 52 H-T-H MOTIF (POTENTIAL).
238 AA, 26802 MW, 9E7ESB7DE6F72CB7 CRC64;
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100.0%; Pred. No. ',
'... 0; Mismatches
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL627272; CAD05488.1; -. EMBL; AE016837; AA068738.1; -. HAMAP; MF.00696; -; 1. InterPro; IPR008220; Fack C. InterPro; IPR000524; HTH_GntR.
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PRINTS; PR00035; HTHGNTR.
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FADR SHEON
Q8ED80;
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Lature 413:852-856(2001).

Represses transcription of at least eight genes required for fatty acid retabolism.

Represses transcription of at least eight genes required for fatty acid transport and beta-oxidation among which fadb, fadb, fadb, fadb, fadb and fadE. Activates transcription of at least three genes con required for unsaturated fatty acid biosynthesis: fabb, fabB and confour for the great encoding the transcriptional regulator of the aceBAK operon encoding the alyoxylate shunt enzymes. Binding of fadR is specifically inhibited by long chain fatty acyl-CoA compounds (By similarity).

Compounds (By similarity).

Compounds (By similarity).

Compounds (By similarity).

Compounds (By similarity).

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InterPro; IPR008920; FadR C.
InterPro; IPR008524; HTH_GhtR.
Pfam; PP00392; ghtR; 1.
PRINTS; PR0035; HTH GNTR; 1.
PROSIDE; S000345; HTH GNTR; 1.
PROSIDE; PROOPOS; HTH GNTR; 1.
PROSIDE; PROOPOS; PROOPOS; PROOPOS; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; PROFICE; P
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
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STRAIN=CO-92 / Biovar Orientalis;
MEDLINE-14704131 PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
15-FALY acid metabolism regulator protein.
PADR OR YPO2144 OR Y2177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE008780; AAL20720.1; -.
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238 AA; 26855 MW;
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NCBI TaxID=632;
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Matches 7; Conservative
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Q8ZEL9;
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RX STRAIN=LAID / Halved registrate in RX STRAIN=LAID / Halved registrate in RX MEDLINE=22137863; PubMed=1214240; RA Perra N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., RA Perra N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., RA Perra N.D., Lindler L.B., Brubaker R.R., Plano G.V., RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., RA Perry R.D.; C. McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., RT Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM."; Genome sequence of Yersinia pestis XIM. Fadb and Genome sequence of Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Yersinia Ye
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EMBL; AF0261; AF0261.
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EMBL; EMBC00822; HTH GATR.
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Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Leatwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
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33 52 H-T-H MOTIF (POTENTIAL).
238 AA; 26770 NW; 27C0885E9767BCD3 CRC64;
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Fatty acid metabolism regulator protein.
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100.0%; Pred. No. ',
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SMART; SM0345; HTH GNTR; 1.
PROSTIE; PS00043; HTH GNTR FAMILY; 1.
PROSTIE; PS0004015m; Transcription regulation; Activator; Repressor;
Patty acid metabolism; Transcription regulation; Activator; Repressor;
DNA-binding; Complete proteome.
HTH GNTR-TYPE.
                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIRE1 TOR Ni6961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Faft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ernolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-22450551; PubMed=12562793;
Herz K., Vimont S., Padan E., Berche P.;
"Roles of NhaA, NhaB, and NhaD Na+/H+ antiporters in survival of
Vibrio cholerae in a saline environment.";
J. Bacteriol. 185:1236-1244(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Fotential).
-!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
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Vibrionaceae, Vibrio.
VGB_TaxID=670,
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34 53 H-T-H MOTIF (POTENTIAL).
279 AA; 31997 MW; 47D710A53CC4F5B1 CRC64;
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InterPro; IPR008920; FadR C.
InterPro; IPR000524; HTH GntR.
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PRINTS; PR00035; HTH
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PROSTIES; PSG0043; HTH GNTR FAMILY; 1.
Fatty acid metabolism; Transcription regulation; Activator; Repressor; DNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                    Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Umayam L.A., Maft D.H., Kolonay J.F., Wandthevan J., Weidman J., Winte O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella Oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Bictechnol. 20:1118-1123(2002).
-!- FUNCTION: Multifunctional regulator of fatty acid metabolism (By
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                                           Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBDNIT: Homodimer (By similarity),
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Protoobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. NCBI TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 240;
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H-T-H MOTIF (POTENTIAL).
; 0EA97D59D7A15EBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.1%; Score 7; DB 1;
100.0%; Pred. No. 7;
iive 0; Mismatches
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Patty acid metabolism regulator protein.
FADR OR VC1900.
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MEDLINE=22297686; PubMed=12368813;
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InterPro; IPR008920; FadR C.
InterPro; IPR000824; HTH GntR.
Pfam; PF00392; GntR; 1.
PRINTS; PR00035; HTHGNTR.
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Best Local Similarity 10v.v.
7; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                   NCBI_TaxID=70863
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                     OR S02885
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Gaps

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Length 279; 0; Indels us-09-856-070b-29.oli.rsp

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HAMAP; MF 00384; -; 1.
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SEQUENCE
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KHSE SULSO
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PROSITE; PS00043; HTH GNTR FAMILY; 1.
Fatty acid metabolism; Transcription regulation; Activator; Repressor; DNA-binding; Complete proteome.
                      MEDLINE-22508454; PubMed=12620739; Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Ijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasuuaga T., Honda T., Shinagawa H., Hattori M., Iida T.; "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholexae."; Lancet 361:743-749(2003).

-!- FUNCTION: Multifunctional regulator of fatty acid metabolism (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Multifunctional regulator of fatty acid metabolism (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                          similarity).
-!- SUBURIT: Homodimer (By similarity) .
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential) .
-!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SUBUNIT: Homodimer (By similarity) .
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential) .
-!- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
NCBL_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               53 H-T-H MOTIF (POTENTIAL).
32069 MW; 8429B92B45149399 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-007-2003 (Rel. 42, Created)
10-007-2003 (Rel. 42, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
18-007-2003 (Rel. 42, Last annotation update)
PADR OR VVI2233.
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Pred. No.
              STRAIN=RIMD 2210633 / Serotype 03:K6;
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InterPro; 1PR008920; FadR_C.
InterPro; IPR000524; HTH_GhtR.
Pfam; PF00392; gntR; 1.
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Best Local Similarity 100...
Try Conservative
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279 AA;
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SEQUENCE FROM N.A.
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DNA BIND
SEQUENCE
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FADR VIBVU
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SERVAINE—21332296; DEM 1617 / P2;

MEDLINE=21332296; DubMed=11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Wehler C.C.-Y., Clausen I.G., Curtis B.A.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-MOGC H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

--- CATALYTIC ACTIVITY: ATP + L-homoserine = ADP + O-phospho-L-
                                                                                                                                                                                                                                                                                                   HAMAP; MF_00696; -; 1.
InterPro; IPR008920; FrdR C.
InterPro; IPR008921; HTH_GntR.
Pfan; PF00392; gntR; 1.
PRINTS; PR0035; HTHGNTR.
SMART; SM00345; HTH GNTR; 1.
FRLY scid metabolism; Transcription regulation; Activator; Repressor;
DNA-binding; Complete protecome.
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-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the GHMP kinase family. Homoserine kinase
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17.1%; Score 7; DB 1; Length 279;

Best Local Similarity 100.0%; Pred. No. 7.9;

Matches 7; Conservative 0; Mismatches 0; Indels
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34 53 H-T-H MOTIF (POTENTIAL).
279 AA, 32072 MW, 733F71C9F1167477 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homoserine kinase (EC 2.7.1.39) (HK).
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Brandell B., C., Bron S.,
Broullet S., Bruschi C.V., Connerton I.F., Cummings N.J., Daniel R.A.,
A. Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Britan K.D., Errington J., Fabret C., Ferrari E., Galleron N.,
A. Fritz C., Pujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A. Hibert H., Holaappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A. Hibert H., Molaappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A. Korayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A. Mollado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Barro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
B. Parro V., Pohl T.M., Potretelle D., Porvollik S., Prescott A.M.,
B. Rieger M., Rivolta C., Roche B., Roche B., Rose M., Sadaie F.,
Aleger M., Rivolta C., Roche B., Roche B., Rose M., Sadaie F.,
Aleger M., Rivolta C., Roche B., Roche B., Rose M., Sadaie F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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MEDLINE=91088245; Pubwed=2124672;
Alonso C., Shirahige K., Ogasawara N.;
"Molecular cloning, genetic characterization and DNA sequence analysis of the recM region of Bacillus subtilis.";
Nucleic Acids Res. 18:6771-6777(1990).
InterPro; IPR006204; GHMP kinase.
InterPro; IPR006203; GHMPknse ATP.
InterPro: IPR008370; Homoser Kin.
Pfam; PF00288; GHMP kinases; I.
PRINTS; PR00958; HOMSERKINASE.
TIGREAMS; TIGR00191; thrB; 1.
PROSITE; PS00627; GHMP KINASES_ATP; 1.
Threonline blosythesis; Transferase; Kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                               Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                      SEQUENCE 311 AA; 33649 MW; 4E39A20E5F83D507 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
DNA polymerase III subunit gamma/tau (BC 2.7.7.7).
DNAX ON DNAH OR BSU00190.
                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
.8.7;
                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  17.1%; Score 7; DB 1
100.0%; Pred. No. 8.7
ive 0; Mismatches
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MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                     ATP
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 1:1-14(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 EEKTKKA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 EEKTKKA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DP3X BACSU
P09122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBDNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. This core dimerizes to form the POLIII' complex. PollII' associates with the gamma complex (composed of gamma, delta, delta', psi and chi chains) and with the beta chain to form the complete DNA polymerase III complex (By similarity).
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takanashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandehol M., Vannier F., Vassarocti A., Viari A., Wambut R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshikawa H.F., Zumsteln E., Yoshikawa H., Danchin A., The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Struck J.C.R., Vogel D.W., Ulbrich N., Erdmann V.A.; "A dnaZX-like open reading frame downstream from the Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase, DNA-directed DNA polymerase, DNA replication, ATP-binding; Complete proteome.
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H -> D (IN REF. 2 AND 3).
2BA428D32B8DC35C CRC64;
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EMBL, D26185; BAA6525.1; --
EMBL, X06803; CAA29958.1; --
EMBL, X52144; CAA36390.1; --
FRIE, X140469; I40469.
PIR; 1134086; I313786.
Subcilist; BG10083; Gnax.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001270; Chaprnin clpA/B.
InterPro; IPR001270; Chaprnin clpA/B.
InterPro; IPR009821; Pol clampload_C.
InterPro; IPR009821; Pol clampload_C.
InterPro; IPR009821; Pol clampload_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subtilis scRNA gene.";
Nucleic Acids Res. 16:2720-2720(1988).
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=168;
MEDLINE=88203213; PubMed=2452406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91002681; PubMed=1698458;
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PRINTS; PR00300; CLPPROTEASEA.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-422 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-5 FROM N.A.
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CONFLICT
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30 RELSEQI 36

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MEDLINE-22608298; PubMed=12665801;
MEDLINE-22608298; PubMed=12665801;
MEDLINE-22608298; PubMed=12665801;
Geraert K., Goethals M., Martens L., Van Damme J., Staes A.,
Thomas G.R., Vandekerckhove J.;
"Exploring proteomes and analyzing protein processing by mass
spectrometric identification of sorted N-terminal peptides.";
Nat. Biotechnol. 21:566-569(2003).
I.: FUNCTION: Probably involved in connections of major cytoskeletal
structures to the plasma membrane.
I.: TSSUE SPECIFICITY: In all tissues and cultured cells studied.
I.: TSIMILARITY: Contains I FERM domain.
I.: DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/MSNID363.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=20388557; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H. Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H. Schaefer C.F., Bhat N.K., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., Rabas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Basa S.S., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Bosas S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hyk S.W., Whiting M., Madan A., Young A.C., Shevchenko Y., Buffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Buffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Abnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92020840; PubMed=1924289;
Lankes W.T., Furthmayr H.;
"Moesin: a member of the protein 4.1-talin-ezrin family of proteins.";
Proc. Natl. Acad. Sci. U.S.A. 88:8297-8301(1991).
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 1-15; 53-59 AND 413-434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Howden P.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Moesin (Membrane-organizing extension spike protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences.
                                                                                                                                                                            STANDARD;
315 RELSEQI 321
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                            HUMAN
                                                                                                                  RESULT 14
MOES_HUMAN
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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SERAINE-NOD; TISSUE-Thymus;
MEDLINE-22354683; PubMed=12466851;
MEDLINE-22354683; PubMed=12466851;
MEDLINE-22354683; PubMed=12466851;
MEDLINE-22354683; PubMed=12466851;
Mikaido I., Osaro N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Nikaido I., Osaro N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Baldarelli R., Tanapin D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Dalla B., Dragani T.A., Fleccher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A gene family consisting of ezrin, radixin and moesin. Its specific localization at actin filament/plasma membrane association sites."; J. Cell Sci. 103:131-143(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93055012; PubMed=1429901;
Sato N., Funayama N., Nagafuchi A., Yonemura S., Tsukita S.,
Tsukita S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 576;
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576 AA; 67689 MW; 96CE7C28D55A8176 CRC64;
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U-MAY-1992 (Rel. 22, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Moesin (Membrane-organizing extension spike protein)
                                                                                                                                                                                                                                                                                                                                                              Structural protein; Cytoskeleton; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                            17.1%; Score 7; DB 1;
100.0%; Pred. No. 14;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 AA
                                          EMBL; M69066; AAA36322.1; -.
EMBL; 298946; CAB46379.1; -.
EMBL; BC017293; AAH17293.1; -.
PIR; A41289; AA41289.
PDB; 1E5W; 27-JUN-01.
PDB; 1EF1; 10-MAY-00.
                                                                                                                                                                                                                                                                                                PRINTS; PR00935; BAND41.
SMART; SM0295; B41; 1.
PR03ITE; P800660; FERM_1; 1.
PR0SITE; P800661; FERM_2; 1.
PR0SITE; P850067; FERM_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity luve.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 REKEELM 347
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MOES_MOUSE
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MGD; MGI:97167; Msn. InterPro; IPR000299; Band 4.1. InterPro; IPR000798; Ez/räd/moesin. InterPro; IPR0008954; Moesin. Pfam; PF00373; Band 41; 1.

EMBL; AK088336; BAC40290.1; -. EMBL; BC047366; AAH47366.1; -.

EMBL; S47577; AAA11762.1;

AAA39728.1;

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RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Rondagya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
R. Retrowsky N., Pillaia R., Pontius J.U., Ol., Ramachandram S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Fingwald M.,
Ravasi T., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Raltana R., Wagner L., Wahlested C.A., Setou M., Shimada K.,
A Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
Ran Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
A Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
A Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,
A Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
A Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
A Hara A., Hashizume W., Imotani K., Shibata K., Shinagawa A.,
A samushi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Manaysis of the mouse transcriptome based on functional annotation of
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RA STRAIN=FVBAN, TISSUE=Breast tumor;

RX MEDINE=2538825; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Shuler G.D.,

RA Alacanla S.P., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Alacanla S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

RA Alacanla R.F., Jordan H., Moretow K.H., Schaefer C.F., Bhar N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malack J.A., Gunarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gaipbs R.A.,

Nilalon D.K., Munny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

RA Hillards M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S. N., Krzzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S. N., Krzzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S. N., Krzzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length

Physical Research A., Schein J.E.,

RA Schein J. R. A., Schein J. L. A., J. A., Schein L. A., Schein L. J. A., Schein L. A., Schein L. J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J. A., J
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MEDLINE=92243764; PubMed=1573844;
Purthmayr H., Lankesw W.R.,
Mosein, a new cytoskeleral protein and constituent of filopodia: its
role in cellular functions.";
Kidney Int. 41:665-670(1992).
-!- FUNCTION: Probably involved in connections of major cytoskeletal
structures to the plasma membrane.
-!- SIMILARITY: Contains 1 FERM domain.
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                                                                                                                                                           Gaps
                                                                                                                                                            0
                                                                                                                                      Length 576;
                                                                                                                                                           0; Indels
                                                                                           EL -> DV (IN REF. 4).

RA -> SP (IN REF. 4).

5E0F4555552E9145 CRC64;
                                                                                                                                       DB 1;
                             PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
Structural protein; CyToskeleton.
DINIT MET 0 0 BY SIMILARITY.
DOMAĪN 1 294 FERM.
                                                                                                                                       Score 7; DB 1;
Pred. No. 14;
                                                                                                                                               100.0%; Pred. No.
                                                                                                                                                                                                                              completed: August 16, 2004, 09:55:16
ne : 33 secs
                                                                                                                   67635 MW;
                                                                                                                                        17.18;
                                                                                                                               Query Match
Best Local Similarity 100.0
....nes 7; Conservative
Pfam; PF00769; ERM; 1.
PRINTS; PR00935; BAND41
SMART; SM00295; B41; 1.
                                                                                                                                                                                                      341 REKEELM 347
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                                                                                                                  576 AA;
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                                                                                            CONFLICT
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Job time
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Mon Aug 16 10:46:51 2004
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August 16, 2004, 09:52:37; Search time 36 Seconds (without alignments) 359.340 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		Description	Q9ujz7 homo sapien	Q9ujz6 homo sapien	Q9ujz8 homo sapien	Q9uk20 homo sapien	Q9ujz2 homo sapien	Q8cbu4 mus musculu	Q8vhk3 rattus norv	Q89k21 bradyrhizob	Q9g103 sus scrofa	Q8suwl encephalito	Q9zew2 enterobacte	Q56576 vibrio algi	Q9c673 arabidopsis	Q9brx7 homo sapien	Q975al sulfolobus	Q8wv17 homo sapien
	oke.	ID	Q9UJZ7	Q9UJZ6	990028	Q9UK20	Q9UJZ2	Q8CBU4	Q8VHK3	Q89K21	O9GL03	QBSUW1	Q9ZEW2	Q56576	090673	Q9BRX7	Q975A1	Q8WV17
		DB	4,	4	4,	4	4	11	11	16	9	ហ	N	N	10	4	17	4
		Query Match Length DB	158	159	156	161	152	421	455	547	578	901	65	128	142	146	181	195
		Query Match	48.8	48.8	46.3	46.3	43.9	29.3	29.3	19.5	19.5	19.5	17.1	17.1	17.1	17.1	17.1	17.1
		Score	20	20	19	19	18	12	12	80	80	80	7	7	7	7	7	7
		Result No.		7	М	4	S	9	7	œ	σ	10	11	12	13	14	15	16

Q9h611 homo sapien Q8zm57 salmonella Q7uet6 rhodopirell Q8bj72 mus musculu Q8c2t7 mus musculu Q97um3 sulfolobus	mus mus coxi schiz	omo omo ritl	Q8bbs3 nome septen Q8bsj2 mus musculu Q8rac1 thermoanaer Q9pt71 xenopus lae Q89y15 bradyrhizob	xant mus homo	Q80w44 mus musculu Q80sx8 mus musculu O83538 treponema p Q8pu38 methanosarc Q9bwu0 homo saplen
266 4 Q9H611 266 16 Q8ZM57 267 16 Q7UET6 272 11 Q8B772 301 11 Q6CZT7	3 11 12	4 4 6 11	510 4 Q96BS3 521 11 Q8BSJ2 566 16 Q8RAC1 580 13 Q9PT71 581 16 Q89VL5	1411	650 11 Q80W44 650 11 Q80SX8 668 16 Q8553 702 17 Q8FU38 796 4 Q9FWU0
7 17.1 7 17.1 7 17.1 7 17.1 7 17.1 7 17.1 7 17.1 7 17.1 7 17.1		7 17.1 7 17.1 7 17.1 7 17.1			7 17.1 7 17.1 7 17.1 7 17.1 7 17.1
113 118 118 110 110	7	22 28 30 30	# # # # # # # # # # # # # # # # # # #	2 E E E E E E E E E E E E E E E E E E E	4 4 4 4 4 1 2 6 4 4 3

## ALIGNMENTS

RESULT 1

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Gaps
                                                                                                                                Eukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                        TISSUE=Ovary;

TISSUE=Ovary;

Chan Z.C., Fadiel A., Naftolin F.;

Chan Z.C., Fadiel A., Naftolin F.;

Chantted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AFIG8897; AAF03155.1;

R GO; GO:0005856; C:cytcoskeleton;

R InterPro; IPR000299; Band 4.1.

InterPro; IPR000799; EZ/rād/moesin.

R Pfam; PF00769; ERM; 1.

R Pfam; PF00769; ERM; 1.

R Pfam; PF00769; ERM; 1.

R Pfam; PF00769; ERM; 1.

R Pfam; PF00769; ERM; 1.

R Pfam; PF00769; ERM; 1.

R Pfam; PF00769; ERM; 1.

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R Pfam; PF00769; ERM; 1.

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R Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

48.8%; Score 20; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 20; Conservative 0; Mismatches 0; Indels
                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment).
Homo sapiens (Human)
           158 AA.
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 EREKEÇMMREKEELMLRLQD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EREKEOMMREKEELMLRLOD 20
             PRELIMINARY;
             Q9UJZ7;
Q9UJZ7
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RESULT Q9UJZ6 us-09-856-070b-29.oli.rspt

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen Z.C., Fadiel A., Naftolin F.;

"Mutation of cytovillin gene in glioblastoma.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

E BEL, AF190059, AAF03158 1.;

R GO; GO:0005856, C:Cytoskeleton;

R InterPro; IPR000799; Band 4.1.

R Pfan; PF00769; ERFM; 1.

R PROSITE; PS50057; FERM, 3; 1.

NON TER 152

SEQÜENCE 152 AA; 18416 MW; B7FCE817DD2B9291 CRC64;
                                                                                                                                                                                                                                                                                                                 TISSUE-Placenta;
TISSUE-Placenta;
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TISSUE-Placenta;
TISSUE-Placenta;
TISSUE-Placenta;
TISSUE-Placenta;
Tissue to an analysis of exrin gene in cancer cells.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR197552; AADS6713.1; -.
EMC, GO; GO; OOO0595; Band 4.1.
TINCEPRO; IPRO00299; Band 4.1.
TINCEPRO; IPRO00799; ERM; 1.
PFam; PRO0769; ERM; 1.
PFAM; PRO0769; ERM; 1.
PROSITE: PSSO057; FERM 3; 1.
TOWN TER
TOWN TER
SEQÜENCE 161 AA; 19439 MW; SFD6EB910E017099 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.9%; Score 18; DB 4; Length 152; 100.0%; Pred. No. 2.6e-10; Live 0; Mismatches 0; Indels
                         Q9UK20;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytovillin 2 (Fragment).
161 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EREKEOMMREKEELMLRLO 19
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Best Local Similarity 100.0
Matches 18; Conservative
PRELIMINARY;
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                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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TISSUE=Brain;
                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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   29UK20
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Q9UJZ8;
Q9UJZ8;
Q1-LAAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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46.3%; Score 19; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels
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"Mutation of ezrin gene in cancer.";
submitted (SEP-199) to the EMBL/GenBank/DDBJ databases.
EMBL, AF188895; AAR03154.1; -.
GO; GO:0005956; C:cytoskeleton; IEA.
InterPro; IPR000299; Band 4.1.
InterPro; IPR00798; Ez/rad/moesin.
PROSITE; PS50057; FEBM, 3; 1.
                                                                                                                                                                                                                                                                                                                       Fadiel A., Chen Z.C., Naftolin F.;
Fadiel A., Chen Z.C., Naftolin F.;
"Mutation of ezrin gene in cancer.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF189213; AAF03156.1; -.
EMBL; AF189213; AAF03156.1; -.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000799; Ez/rād/moesin.
Pfam; PF00769; ERM; 1.
PROSITE; PSS0057; FERM, 3; 1.
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156 156
156 AA; 19042 MW; 159F5AA684A2C3A6 CRC64;
                                                            01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Ezrin (Fregment)
      159 AA.
      PRT;
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      PRELIMINARY;
                                                                                                                                                                                     Homo sapiens (Human).
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TISSUE=Brain;
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Q9GL03
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The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The Riken Genome Exploration Research Group Phase I & II Team;

The Oil 770 full-length cDNAs.";

The Nature 420:563-573(2002).

R MGD, MGI:8931, Vil2.

R MGD, GO:0005856; C:cytoskeleton; IEA.

R InterPro; IPR000299; Band 4.1.

R InterPro; IPR000299; Band 4.1.

R InterPro; IPR000299; Band 4.1.

R Pfam; Pf00373; Band 41; 1.

R Pfam; Pf00373; Band 41; 1.

R PROSITE; PS00661; FERM 2; 1.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.3%; Score 12; DB 11; Length 421; 100.0%; Pred. No. 0.00063; ive 0; Mismatches 0; Indels
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Gunn-Moore F.U. Tait S., Brophy P.U.;
Gunn-Moore F.U. Tait S., Brophy P.U.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF450298, AAL47844.1; -.
GO; GO:0005856; C:cytcskeleton; IEA.
InterPro; IPR000299; Band_4.1.
InterPro; IPR000799; Band_4.1.
Pfam; PF00773; Band_41; 1.
Pfam; PF00779; Band_41; 1.
PRINTS; PR00955; BANDAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA; 50273 MW; E8D6C0D03F6E7497 CRC64;
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Last annotation update)
                                                                                                                              Last sequence update)
Last annotation update)
                                                                   421 AA
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SeQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Urinary bladder;
MEDLINE=22354683; PubMed=12466851;
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PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
                                                                                                         01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Villin 2 (Fragment).
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hes 12; Conservative
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                                                                   PRELIMINARY;
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                                             Q8CBU4
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                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
BNA Res. 9:189-197(2002).
BMBL, AP005953; BAC502.1; --
GO, GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
GO, GO:0006118; P:electron transport; IEA.
InterPro; IPR006099; Acyl-CoA_dh.
InterPro; IPR006091; Acyl-CoA_dh.
InterPro; IPR006091; Acyl-CoA_dh.
InterPro; IPR006091; Acyl-CoA_dh.
InterPro; IPR006091; Acyl-CoA_dh.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Eutheria, Cetartiodactyla, Suina; Suidae, Sus.
NCBL_TaxID=9823;
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AtpB OR Blil5097.
Bradyrhizobium japonicum.
Bacteria; Proteobacteria: Alphaproteobacteria; Rhizobiales;
29.3%; Score 12; DB 11; Length 455; 100.0%; Pred. No. 0.00067; ive 0; Mismatches 0; Indels
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0.NAR-2001 (TrEMBLrel. 16, Created)

01.NAS-2001 (TrEMBLrel. 16, Last sequence update)

01.UN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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100.0%; Pred. No. 8;
tive 0; Mismatches
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Bam, PF05770; Acyl-CoA_dh, M; DROSITE; PS00072; Acyl-CoA_DH_1; DROSITE; PS00073; Acyl-CoA_DH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bradyrhizobiaceae; Bradyrhizobium
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Period protein (Fragment).
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                           342 REKEELMLRLOD 353
     Query Match 29.3
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                            9 REKEELMLRLQD 20
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NON TER
SEQUENCE
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                     STRANT=FI Boar Large White/Meishan;
STRANT=FI Boar Large White/Meishan;
SKinner T.M., Anderson S.I., Lopez-Corrales N.L., Loudon A.S.,
A Haley C.S., Archibald A.L.;
A Haley C.S., Archibald A.L.;
I "Genetic and physical mapping, expression analysis and partial gene
sequence of pordine Perl.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
I Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
BEL; AJ277735; CACL5393.1;
CO; GO:0004871; Fisignal transducer activity; IEA.
R GO; GO:0007165; P:signal transduction; IEA.
R ThterPro; IPR001619; PAS.
R InterPro; IPR001619; PAS.
R InterPro; IPR00989; PAS. 1.
R SWART; SM00086; PAS; 1.
R SWART; SM00091; PAS; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encephalitozoon cuniculi.
Eukaryota, Fungi, Microsporidia, Unikaryonidae, Encephalitozoon.
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EMBL, ALS90447; CAD25684.1; -.

SO, GO.0003735; Fstructural constituent of ribosome; IEA.

Ribosomal protein; Hypothetical protein.

SEQUENCE 901 AA; 96503 MW, 37CZD28ABF2F3A92 CRC64;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ECU07_1530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%; Score 8; DB 6;
100.0%; Pred. No. 8.4;
tive 0; Mismatches
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Best Local Similarity 100.0%
Matches 8; Conservative
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NON TER 578 578
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Best Local Similarity 100.
Matches 8; Conservative
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Q8SUW1
    ACCOCCOS SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVI
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RESULT 11 Q9ZEW2

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STRAIN=AH14;
MEDLINE=20431899; PubMed=10974114;
Osborn A.M., Da Silva Tatley F.M., Steyn L.M., Pickup R.W.,
Osborn A.W.,
Saunders J.R.;
"Mosaic plasmids and mosaic replicons: evolutionary lessons from the analysis of genetic diversity in IncFII-related replicons.";
Microbiology 146:257-2275 (2000).
Microbiology 146:257-2275 (2000).
GG, GO:0046821; C:extrachromosomal DNA, IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                  Plasmid pLV1402.
Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
NCBI_TaxID=61648;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Multifunctional regulator of fatty acid metabolism (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio alginolyticus.
Bateriai, Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=663;
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SMART; SM00345; HTH GNTR; 1.
PROSITE; PS00043; HTH GNTR FAMILY; 1.
DNA-binding; Transcription; Transcription regulation.
NON TER 128 AB: 14.4.
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                               Created)
Last sequence update)
Last annotation update)
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100.0%; Pred. No. 14;
tive 0; Mismatches
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65 AA
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MEDLINE=96332623; PubMed=8695633;
                             01-MAY 1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2003 (TrEMBLrel. 24, CopB (Fragment).
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Best Local Similarity luv...
7; Conservative
                                                                                                                  Enterobacter intermedius.
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 PRELIMINARY;
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Search completed: August 16, 2004, 09:56:03
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Q975A1
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                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                          Length 128;
                                                                                   0; Indels
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PIR; C86389; C66389.
Hypothetical protein.
SEQUENCE 142 AA; 17315 MW; 4DD3225FD6D609B7 CRC64;
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01-UN-2003 (TrEMBLrel. 17, Last sequence update)
11-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Histone deacetylase 6)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
           17.1%; Sco...
100.0%; Pred. No. ...
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Best Local Similarity 100.
                             Query Match 17.1
Best Local Similarity 100.
Matches 7; Conservative
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Gorgosossa S. 1198655061;

GO: GO: 000556;

Finucleic acid binding; IEA.
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                                                                                                                                SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Kalnine M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan M., Farmer A.;
"Cloning of human full-length CDSs in BD Creator(IM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
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                                                                    Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 vector.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 protein, Complete proteome.
181 AA; 20506 MW; 189F3BC6D019FF55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16399 MW; 6A2C1261CE1F83EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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100.0%; Pred. No. 27;
iive 0; Mismatches
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Pred. No.
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EMBL, BC011498, AAH1498.1;
EMBL, BC006649, AAP13595.1;
Interpro, IPR000286, His deacetylse.
Pram, PF00850, Hist deacetyl;
Hypothetical protein.
SEQUENCE 146 AA, 16399 MW; 6A2C126
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SMART; SM00322; KH; 1.
Hypothetical protein; Comple
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein ST0512.
[1]
SEQUENCE FROM N.A.
TISSUE=Brain, and Muscle;
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Best Local Similarity 100.
7; Conservative
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tes 7; Conserva
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Job time : 37 secs